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Carla Myers
AU 1634
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571-272-0747

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Patent Family: _____
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OM protein - protein search, using sw model

Run on: December 20, 2004, 15:41:19 ; Search time 90 Seconds

(without alignments)
4512.017 Million cell updates/sec

Title: US-08-974-584C-118
Perfect score: 5963
Sequence: 1 MPAPRCRAVRSILRSYRE.....TALEAANPALPSDFKTLID 1132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 120 summaries

Database : A_GeneSeq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5963	100.0	1132	2	AAW6113 Human tel
2	5952	99.8	1132	2	AAW6957 Human tel
3	5952	99.8	1132	2	AAW90251 Human cat
4	5952	99.8	1132	2	AAW28881 Human tel
5	5952	99.8	1132	2	AAV32090 Human tel
6	5952	99.8	1132	2	AAV43621 A human t
7	5952	99.8	1132	2	AAV26580 Human tel
8	5952	99.8	1132	4	AAW64859 Heart mus
9	5952	99.8	1132	4	AAW64329 Human pro
10	5952	99.8	1132	4	AAW99930 Human tel
11	5952	99.8	1132	4	AAW82765 Human tel
12	5952	99.8	1132	5	AAE29226 Human tel
13	5952	99.8	1132	5	AAU72735 Human tel
14	5952	99.8	1132	6	ABR42384 Human tel
15	5952	99.8	1132	6	ABR42063 Human tel
16	5952	99.8	1132	6	ABP56676 Human tel
17	5952	99.8	1132	6	ABR56045 Human tel
18	5952	99.8	1132	7	ADDD21420 Human TER
19	5952	99.8	1132	7	ADH72743 Human pro
20	5952	99.8	1132	8	ADG70114 hTERT pro
21	5952	99.8	1132	8	ADG90599 Human TER
22	5952	99.8	1132	8	ADH82172 Human tel
23	5952	99.8	1154	2	AAW61350 Human tel
24	5952	99.8	1189	2	AAW47008 Glutathio
25	5946	99.7	1285	2	AAW47000 H1S tagge

26	5945	99.7	1132	2	AAW71376 Human tel
27	5945	99.7	1132	2	AAV00627 Human tel
28	5945	99.7	1132	2	AAV00638 Human tel
29	5945	99.7	1132	2	AAV28401 Human EST
30	5945	99.7	1132	3	AAV96566 hEST2, a
31	5945	99.7	1132	3	ADc47061 Human TER
32	5945	99.7	1132	7	ADe40482 Human tel
33	5929	99.7	1405	2	AAW56101 Enhanced
34	5918	99.2	1166	2	AAV00647 Telomeras
35	5902.5	99.0	1199	2	AAW47007 Glutathio
36	5873	98.5	1120	2	AAV00641 Telomeras
37	5864	98.3	1120	2	AAV00650 Telomeras
38	5712	95.8	1150	2	AAW47006 Glutathio
39	5546	93.0	1053	2	AAV00640 Altered C
40	5507	92.4	1093	2	AAV00649 Altered C
41	5458	91.5	1041	2	AAV00652 Altered C
42	5458	91.5	1041	2	AAV00643 Altered C
43	5002	83.9	948	2	AAV00639 N-termina
44	4998	83.8	948	2	AAV00648 Truncated
45	4926	82.6	936	2	AAV00642 Truncated
46	4917	82.5	936	2	AAV00651 Truncated
47	4894	82.1	949	2	AAW61349 Human tel
48	4505	75.5	1152	8	ADG90609 hTERT cons
49	4046	67.9	807	2	AAW46897 Human tel
50	4046	67.9	807	2	AAV00637 N-termina
51	4046	67.9	807	2	AAV00646 Truncated
52	3619	60.7	1128	7	ADD21416 Golden ha
53	3619	60.7	1128	8	ADG90603 Hamster T
54	3496	58.6	1122	8	AAV26579 Murine te
55	3496	58.6	1122	8	ADG90601 Murine TE
56	3466	58.1	1122	5	ABW06711 Mouse tel
57	3238	54.3	617	2	AAV00636 N-termina
58	3154	52.9	588	2	AAV00635 N-termina
59	3138	52.6	588	2	AAV00644 N-termina
60	3125	52.4	622	2	AAV25463 Human CRT
61	3038	50.9	591	2	AAW97384 A catalyt
62	2851	44.3	500	6	AAO29840 Human tel
63	2533	41.1	499	6	ABW99678 Amino aci
64	2253	37.8	1131	7	ADD21415 Frog TERT
65	2178	36.5	436	6	ABW99680 Splice va
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67	2167.5	36.3	743	8	ADG90607 Dog TERT
68	2167	36.3	463	6	ABW99679 Splice va
69	2163.5	36.3	437	2	AAV25461 Human CRT
70	2079	34.9	564	2	AAW56109 Human tel
71	2007	33.7	575	8	ADG90605 Rat TERT
72	1863	31.2	348	2	AAV00645 Truncated
73	1541	25.8	538	2	AAW47001 Glutathio
74	1506	25.3	514	2	AAW47004 Glutathio
75	1484	24.9	291	6	AAO29774 hTERT MHC
76	1447	24.3	531	2	AAW47002 Glutathio
77	1438	24.1	283	3	AAV43128 Human tel
78	1417.5	23.8	516	2	AAW47005 Glutathio
79	1338.5	22.4	514	2	AAW47003 Glutathio
80	1293	21.7	520	8	ADG85824 Human tel
81	1090	18.3	259	2	AAW46998 Human tel
82	902	15.1	174	6	AAO29775 hTERT MHC
83	708	11.9	379	4	AAE00431 Consensus
84	667	11.2	174	6	ABW99681 Splice va
85	645	10.8	131	2	AAW97385 Amino aci
86	588	9.9	988	2	AAW56107 S. pombe
87	565	9.5	816	8	ADG70135 HIV RT/hT
88	555	9.3	806	8	ADG70131 HIV RT/hT
89	555	9.3	802	8	ADG70134 HIV RT/hT
90	555	9.3	816	8	ADG70133 HIV RT/hT
91	535	9.0	108	6	ABW99682 Splice va
92	534	9.0	100	5	ABW71628 hTERT tra
93	503	8.4	100	5	ABW71627 hTERT tra
94	478	8.0	576	8	ADG70112 HIV RT/hT
95	478	8.0	592	8	ADG70120 HIV RT/hT
96	478	8.0	605	8	ADG70121 HIV RT/hT
97	461	7.7	816	8	ADG70132 HIV RT/hT
98	459	7.7	456	8	ADG70126 HIV RT/hT

99 459 7.7 462 8 ADG70124 ADG70124 HIV RT/HT
 100 459 7.7 552 8 ADG70123 ADG70123 HIV RT/HT
 101 459 7.7 605 8 ADG70122 ADG70122 HIV RT/HT
 102 452 7.6 586 8 ADG70125 ADG70125 HIV RT/HT
 103 443 7.4 244 4 AAM88748 AAM88748 Human lmm
 104 440.5 7.4 1031 2 AAM56102 AAM56102 Euploies
 105 401 6.7 75 8 ADG70117 ADG70117 hTERT ant
 106 362 6.1 867 7 ADD21426 ADD21426 C alphan
 107 360 6.0 867 4 AAE00423 AAE00423 Candida a
 108 356 6.0 867 4 AAE00424 AAE00424 Candida a
 109 355.5 6.0 864 2 AAM71375 AAM71375 Yeast tel
 110 355.5 6.0 884 2 AAM59778 AAM59778 Amino aci
 111 332.5 5.6 364 2 AAE00430 AAE00430 Schizosac
 112 308 5.2 61 2 AAY00633 AAY00633 Human tel
 113 244 4.1 48 3 AAY6593 AAY6593 Telomeras
 114 239 4.0 48 6 ABB99684 ABB99684 Amino aci
 115 223 3.7 48 2 AAY26581 AAY26581 Peptide s
 116 186 3.1 35 3 AAY6587 AAY6587 Telomeras
 117 184.5 3.1 960 7 ADD21422 ADD21422 G intesti
 118 179.5 3.0 3530 8 ADQ18982 ADQ18982 Human sof
 119 179 3.0 2675 3 AAB07564 AAB07564 Protein e
 120 176 3.0 34 3 AAY6596 AAY6596 Telomeras

ALIGNMENTS

RESULT 1
 ID AAM56113 standard; protein; 1132 AA.
 AC AAM56113;
 DT 13-AUG-1998 (first entry)
 XX
 DE Human telomerase reverse transcriptase protein refined sequence.
 XX
 KM Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 XX cell proliferation; cancer; ageing; ribonucleoprotein.
 OS Homo sapiens.
 XX
 PN GH2317891-A.
 PD 08-APR-1998.
 XX
 PF 01-OCT-1997; 97GB-00020890.
 XX
 PR 01-OCT-1996; 96US-00724643.
 PR 18-APR-1997; 97US-00844419.
 PR 25-APR-1997; 97US-00846017.
 PR 06-MAY-1997; 97US-00851843.
 PR 09-MAY-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00912951.
 PR 14-AUG-1997; 97US-00915503.
 XX
 PA (GERO-) GERO CORP.
 PA (UTTE-) UNIV TECHNOLOGY CORP.
 PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB,
 PI Andrews WH;
 XX
 DR WPI: 1998-171633/16.
 DR N-PSDB; AAV22428.
 XX
 PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.
 XX
 PS Example 1; Fig 74; 387pp; English.
 CC The present sequence represents human telomerase reverse transcriptase

(hTERT), which is a ribonucleoprotein. The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTERT by detecting the change in hTERT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTERT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTERT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTERT and the polynucleotide encoding hTERT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTERT can also be used in the new methods

Sequence 1132 AA;
 50
 Query Match 100.0%; Score 5963; DB 2; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPRAPRCRAVRLSLRSHYREVLPATFRRPLGQGMRLVORGDPAPFALVACLYCPW 60
 1 MPRAPRCRAVRLSLRSHYREVLPATFRRPLGQGMRLVORGDPAPFALVACLYCPW 60
 61 DARPPAPSPFROVSCLEKELVARVLORLCERGAKNVLAFFALDDGARGPPAFITTSVR 120
 61 DARPPAPSPFROVSCLEKELVARVLORLCERGAKNVLAFFALDDGARGPPAFITTSVR 120
 121 SYLENTVTDALRSGANGLLLRVGDVVLHLLARCALFVLVAPSCAYQCGPPLYOLGA 180
 121 SYLENTVTDALRSGANGLLLRVGDVVLHLLARCALFVLVAPSCAYQCGPPLYOLGA 180
 181 ATQARPPHAGSGPRRLCERAMNHSVREAGVPLGAPARRRGGSASLSLPRPRR 240
 181 ATQARPPHAGSGPRRLCERAMNHSVREAGVPLGAPARRRGGSASLSLPRPRR 240
 241 GAAPERTPTVGQSWAPGRTGSPSPGFCVSPAPPAEATSLGALSGTSHSPSVG 300
 241 GAAPERTPTVGQSWAPGRTGSPSPGFCVSPAPPAEATSLGALSGTSHSPSVG 300
 301 ROHHAGPSTSRPPRPMDTPCPVYATKHFLLSSGDKELRPSFLSSRPSLTGARRL 360
 301 ROHHAGPSTSRPPRPMDTPCPVYATKHFLLSSGDKELRPSFLSSRPSLTGARRL 360
 361 VETIFLGSRRPMMPGTPRLPLPQRYWQMRPLFLELGNHAQCPYGVILKTHCPLRAAVT 420
 361 VETIFLGSRRPMMPGTPRLPLPQRYWQMRPLFLELGNHAQCPYGVILKTHCPLRAAVT 420
 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLROHSSPMQVYGFVACRLVLPGLMGS 480
 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLROHSSPMQVYGFVACRLVLPGLMGS 480
 481 RHNERRRFLRNTKKPISLGGKAKLSLOELTWKMSVRCAMLRSPGVCVPAARHRLREEL 540
 481 RHNERRRFLRNTKKPISLGGKAKLSLOELTWKMSVRCAMLRSPGVCVPAARHRLREEL 540
 541 LAKFLHMLSVVYVELRFFYYTETTFQKNRLFPRPSWSKLQSIGRQHLKRYOLRE 600
 541 LAKFLHMLSVVYVELRFFYYTETTFQKNRLFPRPSWSKLQSIGRQHLKRYOLRE 600
 601 LSEAEVQRHEARPAALITSLRFLPKPDGLRFLVMDYVVGATFRERARELTSRVYA 660
 601 LSEAEVQRHEARPAALITSLRFLPKPDGLRFLVMDYVVGATFRERARELTSRVYA 660
 661 LFSVLTNERARRRPGLLGASVLDGLDILHRAVRTFVLVRAQDPPPELHYFVKVDYTGAYDTI 720
 661 LFSVLTNERARRRPGLLGASVLDGLDILHRAVRTFVLVRAQDPPPELHYFVKVDYTGAYDTI 720

QY 721 PODRLTEVIAIITKPONTYCVRRYAVVQKAAHGVKAKFSKSHVSTLTDLOPYWQCFVHL 780
 CC (hTERT) which is a ribonucleoprotein. The present invention also
 CC describes the following methods: (A) determining whether a test compound
 CC is a modulator of hTERT, by detecting the change in hTERT recombinant
 CC protein or polynucleotide, on administration of the compound; (B)
 CC preparation of recombinant telomerase by contacting a protein preparation
 CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
 CC protein in a sample by binding a relevant probe to the sample and
 CC detecting the complex formed or in the case of RNA detection, amplifying
 CC the product and correlating the presence of complex or amplification
 CC product with presence of hTERT in the sample; and (D) increasing the
 CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
 CC the use of an agent that causes an increase in cell vertebrate cell
 CC proliferation to create a medicament that inhibits ageing. A protein
 CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
 CC the manufacture of medicaments for inhibiting the effect of ageing or
 CC cancer. Inhibitors of telomerase activity can be used to treat conditions
 CC that are associated with high telomerase activity. A protein preparation
 CC of hTERT can also be used in the new methods

QY 721 PODRLTEVIAIITKPONTYCVRRYAVVQKAAHGVKAKFSKSHVSTLTDLOPYWQCFVHL 780
 Db 721 PODRLTEVIAIITKPONTYCVRRYAVVQKAAHGVKAKFSKSHVSTLTDLOPYWQCFVHL 780
 QY 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRMCHNAVRIRKSYVQCGIPQGSILSTL 840
 Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRMCHNAVRIRKSYVQCGIPQGSILSTL 840
 QY 841 LCSIQVDMENKIFAGIRRDGLLRIVDDPLVTPHITAKTETRLTGVPEYGVNL 900
 Db 841 LCSIQVDMENKIFAGIRRDGLLRIVDDPLVTPHITAKTETRLTGVPEYGVNL 900
 QY 901 RKTIVNPEVEDEALGTAFAVQMPAHGLFPMCGLLDRTLLEVDSSYARTSIRASVTF 960
 Db 901 RKTIVNPEVEDEALGTAFAVQMPAHGLFPMCGLLDRTLLEVDSSYARTSIRASVTF 960
 QY 961 NRGFKAGNNRRKLFGLRLKCHSLFDLDQVNSIQVCTNIYKILLQANRFACVLOLP 1020
 Db 961 NRGFKAGNNRRKLFGLRLKCHSLFDLDQVNSIQVCTNIYKILLQANRFACVLOLP 1020
 QY 1021 FHQGVWKNPTFFLRVIDSTASLCYSILKAKAGMSLGAKGAPLPSEAVQMLCHQAFLL 1080
 Db 1021 FHQGVWKNPTFFLRVIDSTASLCYSILKAKAGMSLGAKGAPLPSEAVQMLCHQAFLL 1080
 QY 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPSTTLTALMAANPALPSDFKITLD 1132
 Db 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPSTTLTALMAANPALPSDFKITLD 1132

RESULT 2
 AA46957
 ID AA46957 standard; protein; 1132 AA.

AC AA46957;
 XX 13-AUG-1998 (first entry)
 DT 13-AUG-1998 (first entry)
 XX Human telomerase reverse transcriptase.
 DE Human telomerase reverse transcriptase.
 XX Human telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 KM cell proliferation; cancer; ageing; ribonucleoprotein.
 XX Homo sapiens.
 OS Homo sapiens.
 XX GB2317891-A.
 FN 08-APR-1998.
 PD 08-APR-1998.
 XX 01-OCT-1997; 97GB-00020890.
 PE 01-OCT-1997; 97GB-00020890.
 XX 01-OCT-1996; 96US-00724643.
 PR 18-APR-1997; 97US-00844419.
 PR 25-APR-1997; 97US-00846017.
 PR 06-MAY-1997; 97US-00851843.
 PR 09-MAY-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00912851.
 PR 14-AUG-1997; 97US-00915503.
 XX (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX Cecch TR, Linsinger J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 XX WF1; 1998-171633/16.
 DR N-PSDB; AAV22379.
 XX Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.
 XX Claim 3; Fig 17; 387p; English.

XX The present sequence represents human telomerase reverse transcriptase
 CC (hTERT) which is a ribonucleoprotein. The present invention also
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 CC the product and correlating the presence of complex or amplification
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 CC the manufacture of medicaments for inhibiting the effect of ageing or
 CC cancer. Inhibitors of telomerase activity can be used to treat conditions
 CC that are associated with high telomerase activity. A protein preparation
 CC of hTERT can also be used in the new methods

Query Match 99.8%; Score 5952; DB 2; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSILSHYREVLPATFVRRLGPQGMRLVQRGDPAPAFALVAQCLVCVPM 60
 Db 1 MPRAPRCRAVRSILSHYREVLPATFVRRLGPQGMRLVQRGDPAPAFALVAQCLVCVPM 60
 QY 61 DARPPPAAPSPROVQCLKEIVARVQLRCERGAKNVAFGFALLDAGAGPREATTSTVR 120
 Db 61 DARPPPAAPSPROVQCLKEIVARVQLRCERGAKNVAFGFALLDAGAGPREATTSTVR 120
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 Db 121 SYLPNTVTDALRGSGAMGILLRRVGDVVLHLLARCAFLVAPASCAVQVCPPLVQLGA 180
 QY 181 ATQAPPPPHASGPRRLRCERAMNHSVRBAGVPLCLPAPGARRGGSASRSLPLEKRRR 240
 Db 181 ATQAPPPPHASGPRRLRCERAMNHSVRBAGVPLCLPAPGARRGGSASRSLPLEKRRR 240
 QY 241 GAAPBERTPVQGGSMANRGTRGSDRGFCVVSAPAPAEATSTLEGALSGTRHSHPSVG 300
 Db 241 GAAPBERTPVQGGSMANRGTRGSDRGFCVVSAPAPAEATSTLEGALSGTRHSHPSVG 300
 QY 301 ROHHAAPPSTSRPPRPMDTPCPVVAETKHLFLYSSGDKKQLRPSFLSSLRPSTLGAARL 360
 Db 301 ROHHAAPPSTSRPPRPMDTPCPVVAETKHLFLYSSGDKKQLRPSFLSSLRPSTLGAARL 360
 QY 361 VETTFILGSRPMPGTRPRRLPRLPCRYWQMRPLFLELLGNHACCPYVLLKTHCEPRAVVT 420
 Db 361 VETTFILGSRPMPGTRPRRLPRLPCRYWQMRPLFLELLGNHACCPYVLLKTHCEPRAVVT 420
 QY 421 PAAGVCAAREKPGQSVAAPEEEDTDPRRLVOLLROHSSPMQVGYFYACLRRLVPGLMGS 480
 Db 421 PAAGVCAAREKPGQSVAAPEEEDTDPRRLVOLLROHSSPMQVGYFYACLRRLVPGLMGS 480
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 Db 481 RHNERPFLNRTKFTISLGHAKLSTLOELTWKMSVYDCAMLRSSBGVCYPAEHLRLREI 540
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 QY 601 LSEAEVRQREARPALITSRLRFIPKPDGLRPIVNDYVVGARTTRREKARRLTSRYKA 660
 Db 601 LSEAEVRQREARPALITSRLRFIPKPDGLRPIVNDYVVGARTTRREKARRLTSRYKA 660
 QY 661 LFSVNLVERAARRPGLGASVGLDDIHRAMRFVVRVAADPPPELYFVYVNTGAYDTI 720
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Db 661 LFSVLNTERARRPGLLGASVLGLDIDHRAWRPFVLRVRAQDPPELPEYKVDVTGAYDTI 720
Qy 721 PQRRLTEVLASIIKPNQTYCVRRYAVVQRAAGHAKAKSHVSTLTDQPTMRQFVAHL 780
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Db 781 QETSPRLDAVVIQESSSLNEASSGLPDVFLRFMCHAAVIRKGSYVQCGIQQGSLISTL 840
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Db 841 LCSLCYGDMMENKLPAGIRPDGLILRLVDPFLVPLTHAKPFLRTLVGRVPEYGVNLT 900
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Db 901 RKTIVNPFVEDEALGGTAFFQMPAHGLFPMCGLLDTRLTLEQSDPSASARSISATYF 960
Qy 961 NRGFKAGRMRRKLPFVLRKCHSLFLDQVNSLQVCTNIYKILLQAYRFHACVLOLP 1020
Db 961 NRGFKAGRMRRKLPFVLRKCHSLFLDQVNSLQVCTNIYKILLQAYRFHACVLOLP 1020
Qy 1021 FHQGVKNPFFELRVISDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVQWLCHQATLL 1080
Db 1021 FHQGVKNPFFELRVISDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVQWLCHQATLL 1080
Qy 1081 KLTRHRTVTVPLGLSLRTAQQLSRKLPCTTLTALAAANPALPSDFKTIID 1132
Db 1081 KLTRHRTVTVPLGLSLRTAQQLSRKLPCTTLTALAAANPALPSDFKTIID 1132

RESULT 3
AAW90251
ID AAW90251 standard; protein; 1132 AA.
XX AAW90251;
XX
DT 24-MAY-1999 (first entry)
XX
DE Human catalytic telomerase sub-unit protein.
XX
KM Human, catalytic telomerase subunit; therapy; diagnosis; htc; assay;
KM modulator; treatment; inhibit; cellular disorder; death; defect; cancer;
KM ageing; antisense; neoplastic cell; telomerase-related condition;
KM tumour cell.
XX
OS Homo sapiens.
XX
PN WO9859040-A2.
XX
PD 30-DEC-1998.
XX
PF 09-JUN-1998; 98WO-EP003468.
XX
PR 20-JUN-1997; 97DE-01026329.
PR 26-MAR-1998; 98DE-01013274.
PR 14-APR-1998; 98DE-01016496.
XX
PA (FARB) BAYER AG.
XX
PI Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;
XX
DR WPI; 1999-081276/07.
DR N-PSDB; AAV72117.
XX
PT New catalytically active subunit of human telomerase - used in the
PT modulation of telomerase activity, particularly for treating cancer and
PT ageing.
XX
PS Claim 2; Fig 2; 76pp; German.
XX
CC This sequence represents a novel human catalytic telomerase sub-unit
CC (htc). This protein can be used in screening assays to identify

CC modulators of telomerase and/or other pathological processes involving telomerase,
CC death defects and/or ageing (also suitable for this are agents that
CC particularly cancer and ageing (also suitable for this are agents that
CC stimulate, inhibit or mimic the activity of the subunit). Antisense
CC nucleic acids inhibit telomerase action (by binding to specific mRNA),
CC particularly in neoplastic cells and may be expressed in vivo. Antibodies
CC and fragments of the protein, used as probes or primers, are used to
CC diagnose telomerase-related conditions (especially neoplasia) by (i)
CC detecting abnormal levels of the subunit protein in body fluids or
CC tissues or (ii) by measuring the amount of the encoding nucleic acid.
CC Expression of the nucleic acid encoding the subunit mRNA is confined to
CC tumour cells, in contrast to the ubiquitous expression of the telomerase
CC RNA subunit
XX
SQ Sequence 1132 AA;
Query Match 99.8%; Score 5952; D3 2; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MPRAFCRAVRSILRSHREVLPATFVRRLPGQGRNLYVQGDPAFPALVAQCLVCM 60
Db 1 MPRAFCRAVRSILRSHREVLPATFVRRLPGQGRNLYVQGDPAFPALVAQCLVCM 60
Qy 61 DARPPAPSPFROYSCLEIVARVLOLRCERKANVLAQGFALDAGRGPPAFTTSVR 120
Db 61 DARPPAPSPFROYSCLEIVARVLOLRCERKANVLAQGFALDAGRGPPAFTTSVR 120
Qy 121 SYLPTVTDLRSGAGMLLRVGGDYVYHLARCALFLVAPSCAYQCGPYQLGA 180
Db 121 SYLPTVTDLRSGAGMLLRVGGDYVYHLARCALFLVAPSCAYQCGPYQLGA 180
Qy 181 ATQARPPHAGSPRRRLGCERAMNHSVREAGVPLGAPGARRRGSSASRLPLPRPR 240
Db 181 ATQARPPHAGSPRRRLGCERAMNHSVREAGVPLGAPGARRRGSSASRLPLPRPR 240
Qy 241 GAAPERTPTVGGSMNHPRTGPDRCGVVSPAPAEATSLGALSGRRHSPVS 300
Db 241 GAAPERTPTVGGSMNHPRTGPDRCGVVSPAPAEATSLGALSGRRHSPVS 300
Qy 301 ROHHAGPSTSRPPMDTPCPVVAETKAFLYSSQDXQLRPSFLSSLRPSLTGARL 360
Db 301 ROHHAGPSTSRPPMDTPCPVVAETKAFLYSSQDXQLRPSFLSSLRPSLTGARL 360
Qy 361 VETIFLGSRPWMGTPRRLPLQRYWOMRPLLELGNHACQPYVLLKTHCPRLAAT 420
Db 361 VETIFLGSRPWMGTPRRLPLQRYWOMRPLLELGNHACQPYVLLKTHCPRLAAT 420
Qy 421 PAAGVCAREKPGSVAPPEEDTPRLVOLLRQSSPMQVGFVACLRVLPGLMGS 480
Db 421 PAAGVCAREKPGSVAPPEEDTPRLVOLLRQSSPMQVGFVACLRVLPGLMGS 480
Qy 481 RHNERPFLNTKXFFISLGHAKLSLOELTWKSVRDCAMLRSPGVCPAAEHRLREBI 540
Db 481 RHNERPFLNTKXFFISLGHAKLSLOELTWKSVRDCAMLRSPGVCPAAEHRLREBI 540
Qy 541 LAKEFLHMSVYVVELRSPFYETTFQKNRLEFPFSPWSLSLQSIGRHLKRYQLAE 600
Db 541 LAKEFLHMSVYVVELRSPFYETTFQKNRLEFPFSPWSLSLQSIGRHLKRYQLAE 600
Qy 601 LSEAEVQREARAPALLTSRLRPIPKPDGLPIVNDVYVAGARTFRERREARLTSRYVA 660
Db 601 LSEAEVQREARAPALLTSRLRPIPKPDGLPIVNDVYVAGARTFRERREARLTSRYVA 660
Qy 661 LFSVLNTERARRPGLLGASVLGLDIDHRAWRPFVLRVRAQDPPELPEYKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDIDHRAWRPFVLRVRAQDPPELPEYKVDVTGAYDTI 720
Qy 721 PQRRLTEVLASIIKPNQTYCVRRYAVVQRAAGHAKAKSHVSTLTDQPTMRQFVAHL 780
Db 721 PQRRLTEVLASIIKPNQTYCVRRYAVVQRAAGHAKAKSHVSTLTDQPTMRQFVAHL 780
Qy 781 QETSPRLDAVVIQESSSLNEASSGLPDVFLRFMCHAAVIRKGSYVQCGIQQGSLISTL 840

DB 781 QETSPLRDAVVIQSSSLNEASGLFDVFLRFMCHAVRIRGKSYVOCGIPQGSILSTL 840
 QY 841 LGSICGDMENKLPAGIRRDGILLRLVDDPLVTPHLTHAKFTLTVGVEYGCYVNL 900
 DB 841 LGSICGDMENKLPAGIRRDGILLRLVDDPLVTPHLTHAKFTLTVGVEYGCYVNL 900
 QY 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPWCGILLDTLRELVGSDYSYARTISIRASVTF 960
 DB 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPWCGILLDTLRELVGSDYSYARTISIRASVTF 960
 QY 961 NRGFKAGRMNRKLPGLVLRKCHSLPLDLOVNSLOVCTNITIKILLQAVRFHACTVQLP 1020
 DB 961 NRGFKAGRMNRKLPGLVLRKCHSLPLDLOVNSLOVCTNITIKILLQAVRFHACTVQLP 1020
 QY 1021 FHQOVMNPTFFPLRVISDTASLCYSILKAKNAGMSLGAKGAPLPSBAVQWMLCHQAFLL 1080
 DB 1021 FHQOVMNPTFFPLRVISDTASLCYSILKAKNAGMSLGAKGAPLPSBAVQWMLCHQAFLL 1080
 QY 1081 KLTRHRVTYVPLIGSLRTAQTOLSRKLPCTTLTALBAANPALPSDFKTLTD 1132
 DB 1081 KLTRHRVTYVPLIGSLRTAQTOLSRKLPCTTLTALBAANPALPSDFKTLTD 1132

RESULT 4
 AAY28881
 ID AAY28881 standard; protein; 1132 AA.
 AC AAY28881;
 XX 17-JAN-2000 (first entry)
 DT
 XX Human telomerase reverse transcriptase protein.
 DE
 XX Human telomerase reverse transcriptase protein; hTERT; telomerase; hEST2;
 KM catalytic protein component; cell proliferative capacity; DNA primer;
 KM telomerase substrate; telomeric DNA synthesis; cell immortality;
 KM neoplastic phenotype; diagnostic application; prognostic application;
 KM telomerase related condition; cancer; therapeutic agent;
 KM telomerase expression; telomerase activity.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 608 /note= "Corresponds to cdc codon"
 FT
 XX WO9950279-A1.
 PN 07-OCT-1999.
 PD 31-MAR-1999; 99WO-US007160.
 XX 31-MAR-1998; 98US-00052919.
 PR (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 PI Ceeh TR, Linsner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 XX WPI; 1999-610834/52.
 DR N-PSDB; AA208150.
 XX
 PT Antisense polynucleotides for human telomerase reverse transcriptase used
 for diagnosing or treating cancer.
 XX
 PS Claim 2; Fig 2; 31p; English.
 XX
 CC The present sequence is human telomerase reverse transcriptase protein.
 CC This is the catalytic protein component of telomerase and is also
 CC referred to as hEST2. hTERT has the ability to extend a DNA primer that
 CC functions as a telomerase substrate for telomeric DNA synthesis. This

CC correlates with cell proliferative capacity, cell immortality, and the
 CC development of a neoplastic phenotype. Human TERT antisense
 CC oligonucleotides are useful for diagnostic or prognostic applications to
 CC telomerase related conditions, including cancer. They are also useful as
 CC therapeutic agents, for inhibition of telomerase expression and activity
 XX
 SQ Sequence 1132 AA;
 Query Match 99.8%; Score 5952; DB 2; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPARACBAVNSILRSHREVLPATFRRRLGPGGMLVQSGDPAAPALVAQCLVCPW 60
 DB 1 MPARACBAVNSILRSHREVLPATFRRRLGPGGMLVQSGDPAAPALVAQCLVCPW 60
 QY 61 DARPPAPSPROYSCLELVARVLOLCERGANXVLAFGFALLDGAAGGPEAFTTSVR 120
 DB 61 DARPPAPSPROYSCLELVARVLOLCERGANXVLAFGFALLDGAAGGPEAFTTSVR 120
 QY 121 SYLPNTVDALRGSGAKGLLRVGDVVLVHLRQALFVTVVASCAYVQGGPELYQLGA 180
 DB 121 SYLPNTVDALRGSGAKGLLRVGDVVLVHLRQALFVTVVASCAYVQGGPELYQLGA 180
 QY 121 SYLPNTVDALRGSGAKGLLRVGDVVLVHLRQALFVTVVASCAYVQGGPELYQLGA 180
 DB 121 SYLPNTVDALRGSGAKGLLRVGDVVLVHLRQALFVTVVASCAYVQGGPELYQLGA 180
 QY 181 ATQAPPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRSGASRSLPKPRR 240
 DB 181 ATQAPPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRSGASRSLPKPRR 240
 QY 241 GAAPPERTPVQGGWMAHPGRTGSDRGFCVSPAPPAEATSLLEGALSTGTHSHPSVG 300
 DB 241 GAAPPERTPVQGGWMAHPGRTGSDRGFCVSPAPPAEATSLLEGALSTGTHSHPSVG 300
 QY 301 RQNHGPESTSPRPMDTPCPVYAEKTHFLYSGDKEQRPSPILASLSPSLTGARRL 360
 DB 301 RQNHGPESTSPRPMDTPCPVYAEKTHFLYSGDKEQRPSPILASLSPSLTGARRL 360
 QY 361 VETIFLGRPMWPGTFRRLPLRQRYWQMRPLFELGNHAQCPYGVLLKTHCPRAAVT 420
 DB 361 VETIFLGRPMWPGTFRRLPLRQRYWQMRPLFELGNHAQCPYGVLLKTHCPRAAVT 420
 QY 421 PAAGVCAEKPQGSVAAPBEEDTDPRRLVOLLROSSFWQYGFPAALRLVPPGLGGS 480
 DB 421 PAAGVCAEKPQGSVAAPBEEDTDPRRLVOLLROSSFWQYGFPAALRLVPPGLGGS 480
 QY 481 RANERRFLANTKFLSLGKAKLSLOELTWKSVYDCAMLRSPDVGCVPAEHRRLREI 540
 DB 481 RANERRFLANTKFLSLGKAKLSLOELTWKSVYDCAMLRSPDVGCVPAEHRRLREI 540
 QY 541 LAKFLHMLSVYVVELLRSPFYVTEFTTQKNRLFYFRPSVWSKLOISIRGLKVCQJRE 600
 DB 541 LAKFLHMLSVYVVELLRSPFYVTEFTTQKNRLFYFRPSVWSKLOISIRGLKVCQJRE 600
 QY 601 LSEAEVROHREARPALNLSRLRFTPKPDGLPIVMDVVGARTFRREKARLRSRYKA 660
 DB 601 LSEAEVROHREARPALNLSRLRFTPKPDGLPIVMDVVGARTFRREKARLRSRYKA 660
 QY 661 LFSVLYNEBARPGLIGASVIGLDDIHRAMRTFVLRAADPPPELYVKKVDVGYDTI 720
 DB 661 LFSVLYNEBARPGLIGASVIGLDDIHRAMRTFVLRAADPPPELYVKKVDVGYDTI 720
 QY 721 PODRLTEVASTIKQONTYCVARVAVVQKAAGHKKAFKSVSTLTLDQPMRQFVHL 780
 DB 721 PODRLTEVASTIKQONTYCVARVAVVQKAAGHKKAFKSVSTLTLDQPMRQFVHL 780
 QY 781 QETSPLRDAVVIQSSSLNEASGLFDVFLRFMCHAVRIRGKSYVOCGIPQGSILSTL 840
 DB 781 QETSPLRDAVVIQSSSLNEASGLFDVFLRFMCHAVRIRGKSYVOCGIPQGSILSTL 840
 QY 841 LGSICGDMENKLPAGIRRDGILLRLVDDPLVTPHLTHAKFTLTVGVEYGCYVNL 900
 DB 841 LGSICGDMENKLPAGIRRDGILLRLVDDPLVTPHLTHAKFTLTVGVEYGCYVNL 900
 QY 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPWCGILLDTLRELVGSDYSYARTISIRASVTF 960
 DB 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPWCGILLDTLRELVGSDYSYARTISIRASVTF 960

Db 901 RKTIVNFPVDEALGGTAFAVQMPAHGLPFWCGLLDTRLEQVSDSYASTSIRASTLTF 960
 QY 961 NRGFKAGNNRRRLFGVLRKCHSLFLDQVNSLQTVCTNITKILLQYRHHACVLCQP 1020
 Db 961 NRGFKAGNNRRRLFGVLRKCHSLFLDQVNSLQTVCTNITKILLQYRHHACVLCQP 1020
 QY 1021 FHOQVKNPFTFLRVISDTASLCYSILKAKNAGMSIGANGAAGPLPSEAVQWLCHQAFLL 1080
 Db 1021 FHOQVKNPFTFLRVISDTASLCYSILKAKNAGMSIGANGAAGPLPSEAVQWLCHQAFLL 1080
 QY 1081 KLTRHVTYVPLGLSRLTAQTOLSRKLPFTLLTALPAANPALPSEFTILLD 1132
 Db 1081 KLTRHVTYVPLGLSRLTAQTOLSRKLPFTLLTALPAANPALPSEFTILLD 1132
 RESULT 5
 ID AAY32090 standard; protein; 1132 AA.
 XX AAY32090;
 AC AAY32090;
 DT 17-JAN-2000 (first entry)
 XX Human telomerase reverse transcriptase (hTERT).
 DE Human telomerase reverse transcriptase (hTERT).
 KM Telomerase reverse transcriptase; human; hTERT; cell proliferation;
 XX cancer.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO950386-A2.
 PD 07-OCT-1999.
 XX
 PF 31-MAR-1999; 99WO-US007097.
 XX
 PR 31-MAR-1998; 98US-00052864.
 PR 03-AUG-1998; 98US-00128354.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Morin GB;
 XX
 DR MPI; 1999-6:0842/52.
 DR N-PSDB; AA220279.
 PT
 XX
 PT New catalytic polypeptide and polynucleotide, useful for increasing
 XX catalytic activity in a cell.
 PS Claim 13; Fig 1; 24p; English.
 XX
 CC The present sequence represents human telomerase reverse transcriptase
 CC (hTERT). Human telomerase is a target for diagnosing and treating diseases
 CC relating to cell proliferation and senescence, such as cancer, or for
 CC increasing the proliferative capacity of a cell. A claimed method for
 CC increasing the proliferative capacity of a vertebrate cell, especially a
 CC human or other mammalian cell, involves introducing into the cell a
 CC recombinant hTERT polynucleotide encoding an hTERT variant in which
 CC residues 192-323, 200-323, 192-271, 222-240, 415-450, 192-323
 CC and 415-450, or 192-271 and 415-450 of the present sequence are deleted.
 CC A claimed method of preparing recombinant telomerase involves contacting
 CC a recombinant hTERT deletion mutant (as above) with a telomerase RNA
 CC component such that the 2 proteins associate to form a complex capable of
 CC catalysing the addition of nucleotides to a telomerase substrate. A
 CC claimed method for reducing telomerase activity in a cell involves
 CC introducing a recombinant polynucleotide encoding an hTERT variant having
 CC a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or
 CC 1055-1071 of the present sequence
 XX
 SQ Sequence 1132 AA;
 Query Match 99.8%; Score 5952; DB 2; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPRAPCRAVSLRSHRYREVLPLATFVRRLGQGMRLVORGDPAAFRALVAOCLVCPW 60
 Db 1 MPRAPCRAVSLRSHRYREVLPLATFVRRLGQGMRLVORGDPAAFRALVAOCLVCPW 60
 QY 61 DARPAPAPSPROYSCKEIVARYLOLCERGANVLAFCGALLDQAGGPPPAFTTSVR 120
 Db 61 DARPAPAPSPROYSCKEIVARYLOLCERGANVLAFCGALLDQAGGPPPAFTTSVR 120
 QY 121 SYLPTNTYDILRSGGANGLLRLRGDVLVHLARCAFLVLAPEGAYCGSPYLQOLA 180
 Db 121 SYLPTNTYDILRSGGANGLLRLRGDVLVHLARCAFLVLAPEGAYCGSPYLQOLA 180
 QY 181 ATQARPPPHASGPPRRRLGGERAMNHSVREAGVPLGAPAGARRRGASASLPLEKRR 240
 Db 181 ATQARPPPHASGPPRRRLGGERAMNHSVREAGVPLGAPAGARRRGASASLPLEKRR 240
 QY 241 GAPEPERTVGGSMHAPERTGSPDRGCVVSPAPAEATSLGALSGTHSHSPVG 300
 Db 241 GAPEPERTVGGSMHAPERTGSPDRGCVVSPAPAEATSLGALSGTHSHSPVG 300
 QY 301 ROHAGPSTSRPWRPWCPCPVYAETKHFLLYSQDKQOLRPSFLLSLRPSLTGARL 360
 Db 301 ROHAGPSTSRPWRPWCPCPVYAETKHFLLYSQDKQOLRPSFLLSLRPSLTGARL 360
 QY 361 VETIFLGSRPMWMTGTPRLRLPQRYWQMPRLPLSLGNHACQPYVLLKTHCPLEAAT 420
 Db 361 VETIFLGSRPMWMTGTPRLRLPQRYWQMPRLPLSLGNHACQPYVLLKTHCPLEAAT 420
 QY 421 PAAGVCAREKQGSVAAPBEDTDPRLVLQLEQSHSPQVGYFVACLRPLVPSLMS 480
 Db 421 PAAGVCAREKQGSVAAPBEDTDPRLVLQLEQSHSPQVGYFVACLRPLVPSLMS 480
 QY 481 RANRRPLNTKRFISLQKXAKLSLOBLTWKMSVRDCAMLRSPGVCCPAABHRLREI 540
 Db 481 RANRRPLNTKRFISLQKXAKLSLOBLTWKMSVRDCAMLRSPGVCCPAABHRLREI 540
 QY 541 LAKEFLHMLSVVYVELRSPFYVETTPQKNRLEFFRPSWMSLQSIGRQHLKRVQLE 600
 Db 541 LAKEFLHMLSVVYVELRSPFYVETTPQKNRLEFFRPSWMSLQSIGRQHLKRVQLE 600
 QY 601 LSEAEVQHRREARPALITSRLRPIPKPDGLRPIVNDVYVAGARTFERREKAEHLTSRYVA 660
 Db 601 LSEAEVQHRREARPALITSRLRPIPKPDGLRPIVNDVYVAGARTFERREKAEHLTSRYVA 660
 QY 661 LFSVLYNERARRRGLIGASVGLDIDHRAWRTVLVRQDPEPPELYPVKVDVTGAYDT 720
 Db 661 LFSVLYNERARRRGLIGASVGLDIDHRAWRTVLVRQDPEPPELYPVKVDVTGAYDT 720
 QY 721 PQRRLTEVIAIILKPNQTYCVRRYAVVOKAAGHAKAFKSHVSTLTDLPYWRQFVAHL 780
 Db 721 PQRRLTEVIAIILKPNQTYCVRRYAVVOKAAGHAKAFKSHVSTLTDLPYWRQFVAHL 780
 QY 781 QETSPLDVAVITQSSSLNBAASGLFDVLRPMCHNAVIRKGSYVQCGIIRQGSILSTL 840
 Db 781 QETSPLDVAVITQSSSLNBAASGLFDVLRPMCHNAVIRKGSYVQCGIIRQGSILSTL 840
 QY 841 LCLSLCGDMENKLPAGIRRDGLLRIVYDPLVTPPLTAKTFLRTLVGVEYGCVNL 900
 Db 841 LCLSLCGDMENKLPAGIRRDGLLRIVYDPLVTPPLTAKTFLRTLVGVEYGCVNL 900
 QY 901 RKTIVNFPVDEALGGTAFAVQMPAHGLPFWCGLLDTRLEQVSDSYASTSIRASTLTF 960
 Db 901 RKTIVNFPVDEALGGTAFAVQMPAHGLPFWCGLLDTRLEQVSDSYASTSIRASTLTF 960
 QY 961 NRGFKAGNNRRRLFGVLRKCHSLFLDQVNSLQTVCTNITKILLQYRHHACVLCQP 1020
 Db 961 NRGFKAGNNRRRLFGVLRKCHSLFLDQVNSLQTVCTNITKILLQYRHHACVLCQP 1020
 QY 1021 FHOQVKNPFTFLRVISDTASLCYSILKAKNAGMSIGANGAAGPLPSEAVQWLCHQAFLL 1080
 Db 1021 FHOQVKNPFTFLRVISDTASLCYSILKAKNAGMSIGANGAAGPLPSEAVQWLCHQAFLL 1080

XX	13-SEP-1999	(first entry)	
DT			
XX	Human telomerase reverse transcriptase (hTERT) enzyme.		
DE			
XX	Telomerase reverse transcriptase; TERT; mouse; telomere length assay;		
KM	immunogen; enzyme; telomerase-mediated DNA replication; human.		
KM			
XX	Homo sapiens.		
OS			
XX	W09927113-A1.		
FN			
XX	03-JUN-1999.		
PD			
XX			
XX	25-NOV-1998; 98MO-US025211.		
PF			
XX	26-NOV-1997; 97US-00979742.		
FR	16-MAR-1998; 98US-00042460.		
XX			
XX	(GERO-) GERON CORP.		
PA	(YESH) UNIV YESHIVA EINSTEIN COLLEGE.		
XX			
PI	Morin GB, Allsopp R, Dingho R, Greenberg R;		
XX			
DR	WPI; 1999-347722/29.		
XX			
PT	Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and		
PT	nucleic acids.		
XX			
XX	Disclosure; Fig 3; 135pp; English.		
XX			
CC	The invention relates to a mouse telomerase reverse transcriptase (mTERT)		
CC	enzyme. Compositions containing mTERT can be used in telomere length		
CC	assays. Isolated mTERT is useful as an immunogen for the production of		
CC	monoclonal or polyclonal antibodies. The method is useful for assessing		
CC	the degree of purification and identification of new mTERT species, such		
CC	as an mTERT allele, homolog or isoform, or to screen for modulators		
CC	(antagonists and agonists) of telomerase-mediated DNA replication.		
CC	Antagonists and agonists of mTERT can be used to modify the activity of		
CC	other telomerase enzymes such as human TERT (hTERT). The present sequence		
CC	represents a human TERT enzyme		
XX			
SO	Sequence 1132 AA;		
	Query Match 99.8%; Score 5552; DB 2; Length 1132;		
	Best Local Similarity 99.8%; Pred. No. 0;		
	Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0		
QY	1 MPAPRCRAVRSLSHRYEVPLATFPRRLGPGGMRVVGSDPAAPALVAQCLVCPM 60		
DB	1 MPAPRCRAVRSLSHRYEVPLATFPRRLGPGGMRVVGSDPAAPALVAQCLVCPM 60		
QY	61 DAPPPAASFFQVSCLELVARVLQRLCEGANKVLAFGALIDGARGPPPAFTTSVR 120		
DB	61 DAPPPAASFFQVSCLELVARVLQRLCEGANKVLAFGALIDGARGPPPAFTTSVR 120		
QY	121 SYLENVTALGSGGAGWGLLRVGDVVLHLLARCLFVLVAPSCAYVCGSEPLVQLA 180		
DB	121 SYLENVTALGSGGAGWGLLRVGDVVLHLLARCLFVLVAPSCAYVCGSEPLVQLA 180		
QY	181 ATGAPPPPHASGPRRLGGERAMNHSVREAGVPLGLDPAGARRGGSASRLPLPKPRR 240		
DB	181 ATGAPPPPHASGPRRLGGERAMNHSVREAGVPLGLDPAGARRGGSASRLPLPKPRR 240		
QY	241 GAAPPEERLPVQGSNAHGRTRGSDGFCVSPAPPAEATSLLEALSCTHSHSPVG 300		
DB	241 GAAPPEERLPVQGSNAHGRTRGSDGFCVSPAPPAEATSLLEALSCTHSHSPVG 300		
QY	301 RQHAAPPPSTSPRPMDTCCPVYATKHFPLYSSGDKQLRSEFLSLSLRPSTLGARL 360		
DB	301 RQHAAPPPSTSPRPMDTCCPVYATKHFPLYSSGDKQLRSEFLSLSLRPSTLGARL 360		
QY	361 VETIIIGSSPMVGPTRRLPLPQRYWQMRPLFELLGNHAQCPLYGLKTHCPLEAAT 420		
DB	361 VETIIIGSSPMVGPTRRLPLPQRYWQMRPLFELLGNHAQCPLYGLKTHCPLEAAT 420		

Dd	361	VETIFLGRSPMPGTPRLRLPRLYQVMQMRPLFLELLIGNHQAQCYGLVLTKNHCLRAAVT	420
Qy	421	PAAGYCAAEKQGSVAAPAEEDTDPRRLVQLLRQHSSEWQYGVYRACLRLLVPPGLMG	480
Dd	421	PAAGYCAAEKQGSVAAPAEEDTDPRRLVQLLRQHSSEWQYGVYRACLRLLVPPGLMG	480
Qy	481	RHNERRPLRNTKKFKFISLQCKHAKLSDQELTWMSVRDCAWTLRRSGVGCVPAAERLREEI	540
Dd	481	RHNERRPLRNTKKFKTSLQCKHAKLSDQELTWMSVRDCAWTLRRSGVGCVPAAERLREEI	540
Qy	541	LAKFLHLMWSVYVVELLRSPFYVETTFQKRLFFYPBQVSKLSQISGIRQHLRVQLRE	600
Dd	541	LAKFLHLMWSVYVVELLRSPFYVETTFQKRLFFYPBQVSKLSQISGIRQHLRVQLRE	600
Qy	601	LSAEVRQHRERARPAALLTSRLRFLPKPRGGLAPINMVDYVGARFPREPKARBLTSRYKA	660
Dd	601	LSAEVRQHRERARPAALLTSRLRFLPKPRGGLAPINMVDYVGARFPREPKARBLTSRYKA	660
Qy	661	LFPSVLNTERARPPGLGASVLGLDDIHRAMETFLVLRVAQDPPELFFVKYDVTGAQDTI	720
Dd	661	LFPSVLNTERARPPGLGASVLGLDDIHRAMETFLVLRVAQDPPELFFVKYDVTGAQDTI	720
Qy	721	PODRLTEVIASIIKPQNTYCYRRAAVYQKAHGHVREKAFKSHVSTLTDLPYMQFVAHL	780
Dd	721	PODRLTEVIASIIKPQNTYCYRRAAVYQKAHGHVREKAFKSHVSTLTDLPYMQFVAHL	780
Qy	781	QETSPFLDAVAVIEQSSSLINEASSGLFDFVFLRFMGCHAVIRIGKSYVQCOGIPOGSIITLT	840
Dd	781	QETSPFLDAVAVIEQSSSLINEASSGLFDFVFLRFMGCHAVIRIGKSYVQCOGIPOGSIITLT	840
Qy	841	LCSLCYGDMENKLFAGIRPDGLLRLVDDFLVTPHLLTHAKTFRLTVRGYPERGCVNLT	900
Dd	841	LCSLCYGDMENKLFAGIRPDGLLRLVDDFLVTPHLLTHAKTFRLTVRGYPERGCVNLT	900
Qy	901	RKTYVNFVEVEEALGGTAFFVQMPAHGLFPMGGLLDTRTLEVOQSDYSSYARTSIRASYTF	960
Dd	901	RKTYVNFVEVEEALGGTAFFVQMPAHGLFPMGGLLDTRTLEVOQSDYSSYARTSIRASYTF	960
Qy	961	NRGFKAGNMNRKULFGVLRILKCHSLFLDLOVNSLQTVCTNIYKILLILOAVRFHACVILQLP	1020
Dd	961	NRGFKAGNMNRKULFGVLRILKCHSLFLDLOVNSLQTVCTNIYKILLILOAVRFHACVILQLP	1020
Qy	1021	FHQQVKNRPPFEFLAVISDTSLSQYSIILKAKXAGMSLGKGAAGLPSBAVQWMLCHQAFIL	1080
Dd	1021	FHQQVKNRPPFEFLAVISDTSLSQYSIILKAKXAGMSLGKGAAGLPSBAVQWMLCHQAFIL	1080
Qy	1081	KLTRHRVTVYVPLGSLRTAQOTLSRKULPGITTLTALAEAAANPALPSDEFTIIL	1132
Dd	1081	KLTRHRVTVYVPLGSLRTAQOTLSRKULPGITTLTALAEAAANPALPSDEFTIIL	1132
RESULT 8			
ID	AA664859	standard; protein; 1132 AA.	
XX	AC	AA664859;	
XX	XX		
XX	XX	21-SEP-2001 (first entry)	
DE	XX	Heart muscle cell differentiation related protein SEQ ID NO. 31.	
XX	XX	Heart muscle cell; human; cell differentiation; heart disease.	
XX	OS	Homo sapiens.	
XX	FN	W0200148151-A1.	
XX	PD	05-JUL-2001.	
PF	XX	27-DEC-2000; 2000WO-JP009323.	
FR	XX	28-DEC-1999; 99JP-00372826.	

PR 28-FEB-2000; 2000MO-JP001148.
 PR 02-NOV-2000; 2000MO-JP007741.
 XX
 PA (KYOM) KYOMA HAKKO KOGYO KK.
 XX
 PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
 PI Yamada Y;
 XX
 DR WPI: 2001-425656/45.
 DR N-PSDB; AAA46235.
 XX
 PT Cells capable of differentiating into cardiomyocytes and originating in
 PT bone marrow or umbilical blood cells for study of cardiomyocyte
 PT differentiation and treatment of heart disease.
 XX
 PS Claim 87; Page 143-147; 183pp; Japanese.
 XX
 CC The present invention provides cells originating in the human bone marrow
 CC or umbilical blood cells which are capable of differentiating into
 CC cardiomyocytes. These cells are useful in the treatment of diseases
 CC involving heart muscle degeneration, such as myocardial infarction, and
 CC the study of cardiomyocyte differentiation. The present sequence is a
 CC protein described in the exemplification of the invention
 XX
 SQ Sequence 1132 AA;

Query Match 99.8%; Score 5952; DB 4; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRRRAARSLRSHYREVLPLATFVRLGQGMRLVGRGPAAPRAVAQCIVCM 60
 DB 1 MPAPRRRAARSLRSHYREVLPLATFVRLGQGMRLVGRGPAAPRAVAQCIVCM 60
 QY 61 DAPPPAPSPFQVSCLEKELVARVLQRLCRGAKNVAFGAFALLDGRGPPAFTTSVR 120
 DB 61 DAPPPAPSPFQVSCLEKELVARVLQRLCRGAKNVAFGAFALLDGRGPPAFTTSVR 120
 QY 121 SYLPNTVTDLRGSGANGLLIRYGDVVLHLLARCALFVLVAPSCAYQCGPPLVQLGA 180
 DB 121 SYLPNTVTDLRGSGANGLLIRYGDVVLHLLARCALFVLVAPSCAYQCGPPLVQLGA 180
 QY 121 SYLPNTVTDLRGSGANGLLIRYGDVVLHLLARCALFVLVAPSCAYQCGPPLVQLGA 180
 DB 121 SYLPNTVTDLRGSGANGLLIRYGDVVLHLLARCALFVLVAPSCAYQCGPPLVQLGA 180
 QY 181 ATGARPPPHASGPRRLGGERAMNHSVEAGVPLGAPGARRRGGASRLPLPRPR 240
 DB 181 ATGARPPPHASGPRRLGGERAMNHSVEAGVPLGAPGARRRGGASRLPLPRPR 240
 QY 181 ATGARPPPHASGPRRLGGERAMNHSVEAGVPLGAPGARRRGGASRLPLPRPR 240
 DB 181 ATGARPPPHASGPRRLGGERAMNHSVEAGVPLGAPGARRRGGASRLPLPRPR 240
 QY 241 GAAPERTPTVQGSMAHPGRTGSDRGCVVSPAPAEATSLGALSGTRHSHPSVG 300
 DB 241 GAAPERTPTVQGSMAHPGRTGSDRGCVVSPAPAEATSLGALSGTRHSHPSVG 300
 QY 301 RQHHAGPSTSRPPRPMDTCCPPYATKTFILSSGCKELRSLFLSLRPSLTGARL 360
 DB 301 RQHHAGPSTSRPPRPMDTCCPPYATKTFILSSGCKELRSLFLSLRPSLTGARL 360
 QY 301 RQHHAGPSTSRPPRPMDTCCPPYATKTFILSSGCKELRSLFLSLRPSLTGARL 360
 DB 301 RQHHAGPSTSRPPRPMDTCCPPYATKTFILSSGCKELRSLFLSLRPSLTGARL 360
 QY 361 VETIFLGSRRPMPGTGPRRLPLQRYQMRPLFTELIGNAACCPYGLLTKHCPRAAVT 420
 DB 361 VETIFLGSRRPMPGTGPRRLPLQRYQMRPLFTELIGNAACCPYGLLTKHCPRAAVT 420
 QY 421 PAAGVCARERPOGSVAAPBEEDTDPRRLVOLLROHSSFWQVYGFVACLRRLVPGIWS 480
 DB 421 PAAGVCARERPOGSVAAPBEEDTDPRRLVOLLROHSSFWQVYGFVACLRRLVPGIWS 480
 QY 481 RHNEERRFLRTTKFISLGKAKLSLOELTWMSVPCDCAWLRSPGVGCVPAAEHLREEL 540
 DB 481 RHNEERRFLRTTKFISLGKAKLSLOELTWMSVPCDCAWLRSPGVGCVPAAEHLREEL 540
 QY 541 LAKFLHMLSVYVELLRSPFYVETTFQKNRLFFYRPSWSKIOSIGIRQHLKRYQLRE 600
 DB 541 LAKFLHMLSVYVELLRSPFYVETTFQKNRLFFYRPSWSKIOSIGIRQHLKRYQLRE 600
 QY 601 LSEAEVQOHREARFALLTSRLRFIPKPDGLRPIINMMYVVGARTFRREKRAEELTSVKA 660
 DB 601 LSEAEVQOHREARFALLTSRLRFIPKPDGLRPIINMMYVVGARTFRREKRAEELTSVKA 660

QY 661 LFSVLNTERARRPGLLGASVTLGLDIDIRAMRTFVLRYVRAQDPPELYFVKVDVTGAYDTI 720
 DB 661 LFSVLNTERARRPGLLGASVTLGLDIDIRAMRTFVLRYVRAQDPPELYFVKVDVTGAYDTI 720
 QY 721 PODRLTEVIASIIKPONTYCVRRYAVVOKAAGHVRKAKSVSTLTDLOPYMQFVAHL 780
 DB 721 PODRLTEVIASIIKPONTYCVRRYAVVOKAAGHVRKAKSVSTLTDLOPYMQFVAHL 780
 QY 781 QETSPLRAVAVIEOSSSLNEASSGLFDVEFLRPMCHAVRIRKSVQCCGILPQSSILSTL 840
 DB 781 QETSPLRAVAVIEOSSSLNEASSGLFDVEFLRPMCHAVRIRKSVQCCGILPQSSILSTL 840
 QY 841 LCSLCYGMENKLFAGIRBDGLLRLYDDFLVTPHLLTHAKTFLRLVGVPEYGVVNL 900
 DB 841 LCSLCYGMENKLFAGIRBDGLLRLYDDFLVTPHLLTHAKTFLRLVGVPEYGVVNL 900
 QY 901 RKTIVNPFVEDEALGTFVQMPHAGLFPMCGLLDPTLEVOQSDYSYARTSIRASTF 960
 DB 901 RKTIVNPFVEDEALGTFVQMPHAGLFPMCGLLDPTLEVOQSDYSYARTSIRASTF 960
 QY 961 NRGFGAGNMRRKLPFVRLKCHSLFDLOVNSIQVCTNLYKILLQAVRFAVCVQLP 1020
 DB 961 NRGFGAGNMRRKLPFVRLKCHSLFDLOVNSIQVCTNLYKILLQAVRFAVCVQLP 1020
 QY 1021 FHOQVWKNPTFFLRYISDTASLCISILKAKNAGSLGAKGAAPLPSAVQMLCHQAFLL 1080
 DB 1021 FHOQVWKNPTFFLRYISDTASLCISILKAKNAGSLGAKGAAPLPSAVQMLCHQAFLL 1080
 QY 1081 KLTRHRTVYVPLGSLRTAQTQLSRKLPQTTLTLEAANPALPDDFKTIID 1132
 DB 1081 KLTRHRTVYVPLGSLRTAQTQLSRKLPQTTLTLEAANPALPDDFKTIID 1132

RESULT 9

AA64329
 ID AA64329 standard; protein; 1132 AA.

XX AA64329;
 AC
 DT 24-SEP-2001 (first entry)
 XX
 DE Human protein #2.
 XX
 KM Angiogenesis; cardiac; cell differentiating agent; bone marrow;
 XX heart muscle cell; heart disease; human.
 OS Homo sapiens.
 XX
 PN MO200148149-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-FEB-2000; 2000MO-JP001148.
 XX
 PR 28-DEC-1999; 99JP-00372826.
 XX
 PA (KYOM) KYOMA HAKKO KOGYO KK.
 XX
 PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K;
 XX
 DR WPI: 2001-418252/44.
 DR N-PSDB; AAA49601.
 XX
 PT New adult bone marrow-originated cells capable of differentiating into
 PT heart muscle cells, applicable as remedies for various heart diseases
 PT particularly with damaged heart muscle accompanying degeneration.
 XX
 PS Disclosure; Page 128-134; 158pp; Japanese.
 CC The present invention relates to cells isolated from bone marrow, which
 CC are capable of at least differentiating into heart muscle cells. The
 CC cells are applicable as remedies for various heart diseases particularly

CC with damaged heart muscle accompanying degeneration. The present sequence
 CC was used to illustrate the present invention

XX Sequence 1132 AA;

Query Match 99.8%; Score 5952; DB 4; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPPCRAVRSLSRSHREYVLPATFVRRLGPGCRQLVQGRDPAPAFALVAQCICVCPW 60
 Db 1 MPAPPCRAVRSLSRSHREYVLPATFVRRLGPGCRQLVQGRDPAPAFALVAQCICVCPW 60

QY 61 DAPPPAASPFGVSGSLKELVAVLQRLGCRGAKVLAFGALLGARGGPEAFTSVR 120
 Db 61 DAPPPAASPFGVSGSLKELVAVLQRLGCRGAKVLAFGALLGARGGPEAFTSVR 120

QY 121 SYLNTVTDALRSGAMGILLRRVGDVIVHLLARCAFLVIVAPSCAYQVCGPPLVQLGA 180
 Db 121 SYLNTVTDALRSGAMGILLRRVGDVIVHLLARCAFLVIVAPSCAYQVCGPPLVQLGA 180

QY 181 ATQARPPHASPGRRLGGERAMNHSVREAGVPLGIPAGARRGGSASRSLPLKPRR 240
 Db 181 ATQARPPHASPGRRLGGERAMNHSVREAGVPLGIPAGARRGGSASRSLPLKPRR 240

QY 241 GAAPERTPVGGSWAHPRTRGSDRGFCVSPAPAEATSLGALSGTRSHSPSVG 300
 Db 241 GAAPERTPVGGSWAHPRTRGSDRGFCVSPAPAEATSLGALSGTRSHSPSVG 300

QY 301 RQHHAPBETSRPPRWDTCPPEVVAETGFLYSSGDKQLRPSLLSLRSLTGARL 360
 Db 301 RQHHAPBETSRPPRWDTCPPEVVAETGFLYSSGDKQLRPSLLSLRSLTGARL 360

QY 361 VETIFGSRPMMPGTRRLPRLPORVQWRPLFLELGNHACPPGVLLKTCPRAAVT 420
 Db 361 VETIFGSRPMMPGTRRLPRLPORVQWRPLFLELGNHACPPGVLLKTCPRAAVT 420

QY 421 PAAGVCAKPKQGSVAPEEDTDPRLVQLLRQSSPMQVGYFPAACLRILVPPGLWS 480
 Db 421 PAAGVCAKPKQGSVAPEEDTDPRLVQLLRQSSPMQVGYFPAACLRILVPPGLWS 480

QY 481 RHNERFELNKKFSLSGHAKLSLOELTWMKSVDCALRRSPGVGCPAAEHRLREI 540
 Db 481 RHNERFELNKKFSLSGHAKLSLOELTWMKSVDCALRRSPGVGCPAAEHRLREI 540

QY 541 LAKFLHMLSVYVELLRSPFYVTEFFQKNLFFYRPSVMSKQSIGRHLKRVQRE 600
 Db 541 LAKFLHMLSVYVELLRSPFYVTEFFQKNLFFYRPSVMSKQSIGRHLKRVQRE 600

QY 601 LSAEVRQREARPAALTSRLRPIKPDGLRPIVMNDVVGARTRRERARLTSRVKA 660
 Db 601 LSAEVRQREARPAALTSRLRPIKPDGLRPIVMNDVVGARTRRERARLTSRVKA 660

QY 661 LFSVLNERARRPGLGASVLGIDDIHRAMRTFVLVAQDPPPELYEVKVDVTGAYDTI 720
 Db 661 LFSVLNERARRPGLGASVLGIDDIHRAMRTFVLVAQDPPPELYEVKVDVTGAYDTI 720

QY 721 PQDRLETVASIIKPNNTYCVRRYAVVQAAAGHVRKAFKSVSLTLDQPMRFVANH 780
 Db 721 PQDRLETVASIIKPNNTYCVRRYAVVQAAAGHVRKAFKSVSLTLDQPMRFVANH 780

QY 781 QETSPJRDVAVIEOSSSLNEASSGLFDFVLRPMCHAAVIRKSKSVYQCGIPQSSITSL 840
 Db 781 QETSPJRDVAVIEOSSSLNEASSGLFDFVLRPMCHAAVIRKSKSVYQCGIPQSSITSL 840

QY 841 LSLCYGDMENKLPAGIRRDGLLRVLVDFFLLVTHLTHAKTFLRTLVGVEYCVVNL 900
 Db 841 LSLCYGDMENKLPAGIRRDGLLRVLVDFFLLVTHLTHAKTFLRTLVGVEYCVVNL 900

QY 901 RKTUVNFPEDBALGTAFCVQMPAGHLFPMGCLLIDTRTLEQSSYSSYARTSTASVTF 960
 Db 901 RKTUVNFPEDBALGTAFCVQMPAGHLFPMGCLLIDTRTLEQSSYSSYARTSTASVTF 960

QY 961 NRGPKGRNRRKLPGLVRLKCHSLFLDLQVNSLQVCTNITYKILLLOAYRFPACVLOLP 1020
 Db 961 NRGPKGRNRRKLPGLVRLKCHSLFLDLQVNSLQVCTNITYKILLLOAYRFPACVLOLP 1020

QY 1021 FHOQVKNPFPFLRVISDTASLQSYILKAKNAGMSLGARCAAGPLPSEAVQWMLCHQAFLL 1080
 Db 1021 FHOQVKNPFPFLRVISDTASLQSYILKAKNAGMSLGARCAAGPLPSEAVQWMLCHQAFLL 1080

QY 1081 KLTRHRVTYVPLIGSLRTAQTQLSRKLPGTTLTALANANPALPSPFKIILD 1132
 Db 1081 KLTRHRVTYVPLIGSLRTAQTQLSRKLPGTTLTALANANPALPSPFKIILD 1132

RESULT 10
 AAB99930
 ID AAB99930 standard; protein; 1132 AA.
 XX
 AC AAB99930;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Human telomerase protein sequence SEQ ID NO:31.
 XX
 KW Differentiation; heart muscle cell; cytokine; transcription factor;
 KW proliferation; surface antigen; heart disease; cardiomyocyte;
 KW bone marrow; umbilical blood cell; heart muscle degeneration;
 KW myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 FN W0200148150-A1.
 XX
 PD 05-JUL-2001.
 XX
 PE 02-NOV-2000; 2000WO-JP007741.
 XX
 PR 28-DEC-1999; 99JP-00372826.
 PR 28-FEB-2000; 2000WO-JP001148.
 XX
 PA (XYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
 PI Yamada Y;
 XX
 DR WPI, 2001-42665/45.
 DR N-PDSB; AAB44366.
 XX
 PT Cells capable of differentiating into cardiomyocytes and originating in
 PT bone marrow or umbilical blood cells for study of cardiomyocyte
 PT differentiation and treatment of heart disease.
 XX
 PS Claim 146; Page 137-141; 187pp; Japanese.
 CC
 CC The present invention describes cells originating in bone marrow or
 CC umbilical blood cells which are capable of differentiating into
 CC cardiomyocytes. Also described are: (1) cardiomyocytes produced by the
 CC differentiation of the cells; (2) a method for carrying out the
 CC differentiation into cardiomyocytes, regulated by a promotional and/or
 CC inhibitory factor; (3) a method for the differentiation of the cells into
 CC cell types other than cardiomyocytes; (4) drug compositions promoting the
 CC formation of heart muscle and regeneration of heart tissue which contain
 CC the cells; (5) a method for the production of antibodies which recognise
 CC the cells, especially antibodies which recognise a surface antigen on the
 CC cells; (6) a method for screening factors which promote the proliferation
 CC of the cells; (7) a method for immortalising the cells by expressing
 CC telomerase in them; (8) drug compositions for the treatment of heart
 CC disease which contain the immortalised cells; and (9) cell-free
 CC supernatant from the culture of the cells and its use in promoting their
 CC differentiation into cardiomyocytes. The cells are used in the treatment
 CC of diseases involving heart muscle degeneration, such as myocardial
 CC infarction and in the study of cardiomyocyte differentiation. AAB44351 to
 CC AAB44409 and AAB99915 to AAB99935 represent sequences used in the
 CC exemplification of the present invention

FT Peptide 863. .871
/note="HLA-A2.1 binding motif"
FT Peptide 865. .873
/label=p865
FT Peptide 883. .891
/note="HLA-A2.1 binding motif"
FT Peptide 883. .891
/note="HLA-A2.1 binding motif"
FT Peptide 926. .934
/note="HLA-A2.1 binding motif"
FT Peptide 934. .942
/note="HLA-A2.1 binding motif"
FT Peptide 969. .977
/note="HLA-A2.1 binding motif"
FT Peptide 988. .996
/note="HLA-A2.1 binding motif"
FT Peptide 1072. .1080
/note="HLA-A2.1 binding motif"
FT Peptide 1079. .1087
/note="HLA-A2.1 binding motif"
FT Peptide 1095. .1103
/note="HLA-A2.1 binding motif"
FT Peptide 1122. .1130
/note="HLA-A2.1 binding motif"
XX WC200160391-A1.
XX 23-AUG-2001.
XX 15-FEB-2001; 2001WO-US005143.
XX 15-FEB-2000; 2000US-0182685P.
XX 15-FEB-2001; 2001US-00182685.
XX (REGC) UNIV CALIFORNIA.
XX Zaneetti M;
XX WPI; 2001-536552/59.
XX
XX Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,
PT for treating cancers or tumors or for inducing immune response against
PT tumors, comprises a telomerase reverse transcriptase peptide.
XX
XX Disclosure; Fig 5; 52pp; English.
XX
XX The present sequence is that of human telomerase reverse transcriptase
CC (hTERT). The sequence was analysed for 9-mer peptide sequences containing
CC known binding motifs for the human leukocyte antigen HLA-A2.1 molecule.
CC From an initial panel of about 30 candidate peptides, 2 sequences,
CC denoted p540 (see AAB82772) and p865 (see AAB82773), were examined. The
CC majority of healthy individuals as well as patients with prostate cancer
CC immunised in vitro against these 2 HLA-A2.1 restricted peptides developed
CC hTERT-specific cytotoxic T lymphocytes (CTL). The cancer patients' CTL
CC specifically lysed a variety of HLA-A2+ cancer cell lines such as
CC prostate, breast, colon, lung and melanoma, demonstrating immunological
CC recognition of endogenously-processed hTERT peptides. In vivo immunisation
CC of HLA-A2.1 transgenic mice generated a specific CTL response against
CC both hTERT peptides. The induction of CTL responses in vitro and in vivo,
CC and the susceptibility to lysis of tumour cells of various origins by
CC hTERT CTL suggest that hTERT could serve as a universal cancer vaccine for
CC humans. Thus, a claimed universal vaccine for treating tumours of any
CC origin comprises at least 1 hTERT peptide in an amount effective for
CC initiating and enhancing a CTL response against cancer cells. The peptide
CC is 7-15 amino acid residues in length and may be modified to enhance
CC binding to the major histocompatibility complex. Also claimed is a method
CC for inducing and enhancing a CTL response against cancer cells, involving
CC harvesting blood leucocytes, pulsing with hTERT and contacting cancer
CC cells with the pulsed leucocytes. A method for targeting CTL to tumour
CC cells is also claimed, and involves administering a hTERT peptide to a
CC mammal, especially a cancer patient
XX
XX Sequence 1132 AA;

Query Match 99.8%; Score 5952; DB 4; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPRAKRAVRSILRSYREVLPATFVRRLGSGQWLVORGGPAPAFRAIVACLCVWP 60
1 MPRAKRAVRSILRSYREVLPATFVRRLGSGQWLVORGGPAPAFRAIVACLCVWP 60
DB 1 MPRAKRAVRSILRSYREVLPATFVRRLGSGQWLVORGGPAPAFRAIVACLCVWP 60
QY 61 DARPAPAPSPRQVSCUKELVAVRLORLCERGAKNVLAFAFGALLDGRGPPPAFTTSVR 120
61 DARPAPAPSPRQVSCUKELVAVRLORLCERGAKNVLAFAFGALLDGRGPPPAFTTSVR 120
DB 61 DARPAPAPSPRQVSCUKELVAVRLORLCERGAKNVLAFAFGALLDGRGPPPAFTTSVR 120
QY 121 SYLPTVTDALRSGAGMLLRVGDVYVHLARCLFVLVAPSCAYQCGPILYOLA 180
121 SYLPTVTDALRSGAGMLLRVGDVYVHLARCLFVLVAPSCAYQCGPILYOLA 180
DB 121 SYLPTVTDALRSGAGMLLRVGDVYVHLARCLFVLVAPSCAYQCGPILYOLA 180
QY 181 ATOARPPPHASGPRRLGCEPAMNHSYREAGVPLGAPAPARAGSASRLPLKPRR 240
181 ATOARPPPHASGPRRLGCEPAMNHSYREAGVPLGAPAPARAGSASRLPLKPRR 240
DB 181 ATOARPPPHASGPRRLGCEPAMNHSYREAGVPLGAPAPARAGSASRLPLKPRR 240
QY 241 GAAPERPRTVGGQSWAHPGRTGSPDRGCVVSPAPAEATSLGALSGTSHSPVG 300
241 GAAPERPRTVGGQSWAHPGRTGSPDRGCVVSPAPAEATSLGALSGTSHSPVG 300
DB 241 GAAPERPRTVGGQSWAHPGRTGSPDRGCVVSPAPAEATSLGALSGTSHSPVG 300
QY 301 ROHHAGPSTSRPMPDTPCPVVAETKHFVLSGSGDEQLRPSFLSSLRPSLTGARL 360
301 ROHHAGPSTSRPMPDTPCPVVAETKHFVLSGSGDEQLRPSFLSSLRPSLTGARL 360
DB 301 ROHHAGPSTSRPMPDTPCPVVAETKHFVLSGSGDEQLRPSFLSSLRPSLTGARL 360
QY 361 VETIFLGSRPMPGTPRRLPLRQRYWQMPLEFLIGNHAQCPYVLLKTHCPLEAAVT 420
361 VETIFLGSRPMPGTPRRLPLRQRYWQMPLEFLIGNHAQCPYVLLKTHCPLEAAVT 420
DB 361 VETIFLGSRPMPGTPRRLPLRQRYWQMPLEFLIGNHAQCPYVLLKTHCPLEAAVT 420
QY 421 PANGVCAREKQGSVAPEEDTDPRIYOLRQHSPPQVYGFVACLRPLVPPGLMS 480
421 PANGVCAREKQGSVAPEEDTDPRIYOLRQHSPPQVYGFVACLRPLVPPGLMS 480
DB 421 PANGVCAREKQGSVAPEEDTDPRIYOLRQHSPPQVYGFVACLRPLVPPGLMS 480
QY 481 RHNERRFLRNTKKFISLGKXKLSLOELTWKMSVRDCAMLRSPGVGCVPAAEHRLREI 540
481 RHNERRFLRNTKKFISLGKXKLSLOELTWKMSVRDCAMLRSPGVGCVPAAEHRLREI 540
DB 481 RHNERRFLRNTKKFISLGKXKLSLOELTWKMSVRDCAMLRSPGVGCVPAAEHRLREI 540
QY 541 LAKFLHMLSVYVELLSRFYTTETTPQKNRLFRRPSVWSLQSIGRQHKRQVLE 600
541 LAKFLHMLSVYVELLSRFYTTETTPQKNRLFRRPSVWSLQSIGRQHKRQVLE 600
DB 541 LAKFLHMLSVYVELLSRFYTTETTPQKNRLFRRPSVWSLQSIGRQHKRQVLE 600
QY 541 LAKFLHMLSVYVELLSRFYTTETTPQKNRLFRRPSVWSLQSIGRQHKRQVLE 600
541 LAKFLHMLSVYVELLSRFYTTETTPQKNRLFRRPSVWSLQSIGRQHKRQVLE 600
DB 541 LAKFLHMLSVYVELLSRFYTTETTPQKNRLFRRPSVWSLQSIGRQHKRQVLE 600
QY 601 LSEAEVQREARPAALTSRLRFIPKPDGLRPLVNMNDYVGARTFPEREARELTSRYVA 660
601 LSEAEVQREARPAALTSRLRFIPKPDGLRPLVNMNDYVGARTFPEREARELTSRYVA 660
DB 601 LSEAEVQREARPAALTSRLRFIPKPDGLRPLVNMNDYVGARTFPEREARELTSRYVA 660
QY 661 LFSVLYTERARRPGLIGASVLTGDDIHRAMRTFVLKRAQDEPPELYFVKVDYTGAVDTI 720
661 LFSVLYTERARRPGLIGASVLTGDDIHRAMRTFVLKRAQDEPPELYFVKVDYTGAVDTI 720
DB 661 LFSVLYTERARRPGLIGASVLTGDDIHRAMRTFVLKRAQDEPPELYFVKVDYTGAVDTI 720
QY 721 PODRLTEVIAIIRKQNTYCVRRYAVVQKAAHGVKAPKSHVSTLTDLQPYMRGVAIL 780
721 PODRLTEVIAIIRKQNTYCVRRYAVVQKAAHGVKAPKSHVSTLTDLQPYMRGVAIL 780
DB 721 PODRLTEVIAIIRKQNTYCVRRYAVVQKAAHGVKAPKSHVSTLTDLQPYMRGVAIL 780
QY 781 QETSPLADAVVIBQSSSLNEASGLFDVLFREYCHHAVIRKGSYVQCGIPIQGSILSTL 840
781 QETSPLADAVVIBQSSSLNEASGLFDVLFREYCHHAVIRKGSYVQCGIPIQGSILSTL 840
DB 781 QETSPLADAVVIBQSSSLNEASGLFDVLFREYCHHAVIRKGSYVQCGIPIQGSILSTL 840
QY 841 LCLSLCGDMENKLPAGIRBRGILLRLVDEPLVTPBLTAKFTLRTLVGVEYGVNVL 900
841 LCLSLCGDMENKLPAGIRBRGILLRLVDEPLVTPBLTAKFTLRTLVGVEYGVNVL 900
DB 841 LCLSLCGDMENKLPAGIRBRGILLRLVDEPLVTPBLTAKFTLRTLVGVEYGVNVL 900
QY 901 RKTIVVFPVEDDELGTAFAVQMPAHGLFPMCGILLDTRTLLEVQSDVYSARISIRASVTF 960
901 RKTIVVFPVEDDELGTAFAVQMPAHGLFPMCGILLDTRTLLEVQSDVYSARISIRASVTF 960
DB 901 RKTIVVFPVEDDELGTAFAVQMPAHGLFPMCGILLDTRTLLEVQSDVYSARISIRASVTF 960
QY 961 NRGFKAGRMNRKLFGLVLRKCHSLDLQVNSLQVCTNIIKILLQAYRHACTLQUP 1020
961 NRGFKAGRMNRKLFGLVLRKCHSLDLQVNSLQVCTNIIKILLQAYRHACTLQUP 1020
DB 961 NRGFKAGRMNRKLFGLVLRKCHSLDLQVNSLQVCTNIIKILLQAYRHACTLQUP 1020
QY 1021 FHOQVKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSBAVOMLCHQAFLL 1080
1021 FHOQVKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSBAVOMLCHQAFLL 1080

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Db 1021 FHQVWKNPFFLIVISDTASLCSILKAKAGMSLGAKGAGPLPSEAVQWMLCHOAFL 1080
Qy 1081 KLTFRHTVYVPLGLSLTACTOISRKLPSTTLTALEAANPALPSDFKTIID 1132
Db 1081 KLTFRHTVYVPLGLSLTACTOISRKLPSTTLTALEAANPALPSDFKTIID 1132

RESULT 12
ID AAE29226 standard; protein; 1132 AA.
XX AAE29226
AC AAE29226;
XX
XX 27-JAN-2003 (first entry)
XX
XX Human telomerase reverse transcriptase (TERT).
XX
XX Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
XX transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
XX telomerase reverse transcriptase.
XX
XX Homo sapiens.
XX
XX MO200274948-A2.
XX
XX 26-SEP-2002.
XX
XX 21-MAR-2002; 2002WO-CA000378.
XX
XX 21-MAR-2001; 2001US-0277811P.
XX
XX (GERO-) GERON CORP.
XX
XX Denning C, Clark AJ, Schiff JM;
XX
XX WPI; 2002-759895/82.
XX
XX N-PSDB; AAD46821.
XX
XX Mammalian cells, useful for producing animal tissues with carbohydrate
XX antigens that are compatible for transplantation into human patients.
XX
XX Disclosure; Page 34; 71pp; English.
XX
XX The invention relates to animal tissues with carbohydrate antigens that
XX are compatible for transplantation into human patients. The mammalian
XX cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
XX transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
XX fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
XX with carbohydrate antigens that are compatible for transplantation into
XX human patients. The present sequence is human telomerase reverse
XX transcriptase (TERT) used in the invention
XX
XX Sequence 1132 AA:
SQ
Query Match 99.8%; Score 5952; DB 5; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 181 ATOARPPHAGSPRRRLGCEERAMNHSVEAGVPLGLPAPGARRRGGASASLPLPKRPR 240
Qy 241 GAAPPEPRTPVQGSMAHPRGTRGSPDRGFCVVSAPRAEEXTSLGALSGTRHSPVSG 300
Db 241 GAAPPEPRTPVQGSMAHPRGTRGSPDRGFCVVSAPRAEEXTSLGALSGTRHSPVSG 300
Qy 301 ROHHAAGPSTSRPPRPMWTPPCPPVYAEFKHPLYSAGDKEQLRPSFLSLGSRBSLTGARL 360
Db 301 ROHHAAGPSTSRPPRPMWTPPCPPVYAEFKHPLYSAGDKEQLRPSFLSLGSRBSLTGARL 360
Qy 361 VETITLFGSSPMWGPBRPLRPLPORWQMRPLFLELNHGOCPGYVLKTHCPRAAVT 420
Db 361 VETITLFGSSPMWGPBRPLRPLPORWQMRPLFLELNHGOCPGYVLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGGSVAAPSEEDTDPRRLVQLRQHSFMYQYGFYRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGGSVAAPSEEDTDPRRLVQLRQHSFMYQYGFYRACLRLVPPGLWGS 480
Qy 481 RNNRRFLRNTKKTSLGKHAQLSTQELTWKMSVDCAMLRSPVGCVPAAHRLREI 540
Db 481 RNNRRFLRNTKKTSLGKHAQLSTQELTWKMSVDCAMLRSPVGCVPAAHRLREI 540
Qy 541 LAKFLHMLMSYVVELLSFFYVETTFQKNRLFYRPSVMSKQSLGIRQHLKRVQURE 600
Db 541 LAKFLHMLMSYVVELLSFFYVETTFQKNRLFYRPSVMSKQSLGIRQHLKRVQURE 600
Qy 601 LSEAEVRQREARPPALTSRLAFIRKPDGLRPIVMQDYVGARTRRKRAERLTRYKA 660
Db 601 LSEAEVRQREARPPALTSRLAFIRKPDGLRPIVMQDYVGARTRRKRAERLTRYKA 660
Qy 661 LFSVLYNERARPPGLGASVGLDDIHRAMRTFVLRVAQDPPPELTVKQDVTGAYDTI 720
Db 661 LFSVLYNERARPPGLGASVGLDDIHRAMRTFVLRVAQDPPPELTVKQDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKQNTYCVARYAVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKQNTYCVARYAVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPLEADAVVTEQSSSLNEASSGLFDVFLRMCHAVRIRKGSYVQCGIPOGSLISTL 840
Db 781 QETSPLEADAVVTEQSSSLNEASSGLFDVFLRMCHAVRIRKGSYVQCGIPOGSLISTL 840
Qy 841 LCSLCYGMENKLFAGIRRDGLRLVDDFLVTFPHLTHAKTFRTTVRGVPEYGVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLRLVDDFLVTFPHLTHAKTFRTTVRGVPEYGVVNL 900
Qy 901 RKTIVNFPVEDALAGTAFAVQMPAHGLFPWCGLLIDTTLLEVQSYSSYARTSTAATF 960
Db 901 RKTIVNFPVEDALAGTAFAVQMPAHGLFPWCGLLIDTTLLEVQSYSSYARTSTAATF 960
Qy 961 NRGFKAGRMREKTLGVRLKCHSLFLDQVNSLQTVCTNIYKILLDAQYFHAQVLDLP 1020
Db 961 NRGFKAGRMREKTLGVRLKCHSLFLDQVNSLQTVCTNIYKILLDAQYFHAQVLDLP 1020
Qy 1021 FHQVWKNPFFLIVISDTASLCSILKAKAGMSLGAKGAGPLPSEAVQWMLCHOAFL 1080
Db 1021 FHQVWKNPFFLIVISDTASLCSILKAKAGMSLGAKGAGPLPSEAVQWMLCHOAFL 1080
Qy 1081 KLTFRHTVYVPLGLSLTACTOISRKLPSTTLTALEAANPALPSDFKTIID 1132
Db 1081 KLTFRHTVYVPLGLSLTACTOISRKLPSTTLTALEAANPALPSDFKTIID 1132

RESULT 13
ID AAU72735 standard; protein; 1132 AA.
XX AAU72735;
XX
XX 09-APR-2002 (first entry)
XX
XX Human telomerase reverse transcriptase (TERT).
XX

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KM Telomerase reverse transcriptase; TERT; cytosolic; apoptosis;
KM cell growth inhibitor; antisense oligonucleotide; antisense technology.
XX Homo sapiens.
XX
XX W0200108198-A1.
XX
XX PD 22-NOV-2001.
XX
XX PF 15-MAY-2001; 2001WO-05015774.
XX
XX PR 16-MAY-2000; 2000US-00572423.
XX PR 07-DEC-2000; 2000US-00733294.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Monia BP, Gaarde WA, Freier SM, Wanciewicz E;
XX WPI; 2002-075321/10.
XX DR N-PSDB; AAS96607.
XX
XX PT New compound targeted to nucleic acid molecule encoding telomerase
XX PT expression of TERT, useful for modulating apoptosis and inhibiting cell
XX PT growth.
XX
XX PS Disclosure; Page 100-105; 154pp; English.
XX
XX CC The invention describes a compound, 8-50 nucleobases in length targeted
XX CC to a nucleic acid molecule encoding human TERT (telomerase reverse
XX CC transcriptase), where the compound specifically hybridizes with and
XX CC inhibits the expression of TERT. A series of oligonucleotides were
XX CC designed to target different regions of the human TERT RNA. These were 20
XX CC nucleotides in length and composed of a central gap region consisting of
XX CC ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by
XX CC five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-
XX CC MOE) nucleotides. The compounds were analyzed for their effect on human
XX CC TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction
XX CC (PCR). The compound is useful for inhibiting the expression of TERT in
XX CC cells or tissues, for treating a human having disease or condition
XX CC associated with TERT, for modulating apoptosis, for inhibiting cell
XX CC growth (preferably, cancer cell growth), in antisense therapy and for
XX CC diagnostics and therapeutics. This is the amino acid sequence of human
XX CC telomerase reverse transcriptase (TERT), described in the method of the
XX CC invention
XX
SQ Sequence 1132 AA;
Query Match 99.8%; Score 5952; DB 5; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSILRSHYREVLPATFVRLGPOGRLVQDGPAPAFALVAQCLVCPM 60
DB 1 MPAPRCRAVRSILRSHYREVLPATFVRLGPOGRLVQDGPAPAFALVAQCLVCPM 60
QY 61 DAPPPAAPSFRVQSLKELVARVLOQLCERGAKNVLAFFPALDQAGGPEAFTTSVR 120
DB 61 DAPPPAAPSFRVQSLKELVARVLOQLCERGAKNVLAFFPALDQAGGPEAFTTSVR 120
QY 121 SYLNTVTALRSGSGMGLLRVDDVLAHLLARCALFVLAAPSCAYOVGPPLYOLGA 180
DB 121 SYLNTVTALRSGSGMGLLRVDDVLAHLLARCALFVLAAPSCAYOVGPPLYOLGA 180
QY 181 ATGAPPPAASGPRRLGGERAMNHSVREAGVPLGPAFGARRGSGASRSLLPKRRR 240
DB 181 ATGAPPPAASGPRRLGGERAMNHSVREAGVPLGPAFGARRGSGASRSLLPKRRR 240
QY 241 GAAPFERTPVGGSAHAGRTGPDRCFCVSPAPRAEETSLEGLSGTRSHHPSVG 300
DB 241 GAAPFERTPVGGSAHAGRTGPDRCFCVSPAPRAEETSLEGLSGTRSHHPSVG 300
QY 301 RQHHAGPSTSRPPFMDTPCPFVVAETKGLFLYSSGDKQLRPSFLSLRPSLTGARRL 360

DB 301 RQHHAGPSTSRPPFMDTPCPFVVAETKGLFLYSSGDKQLRPSFLSLRPSLTGARRL 360
QY 361 VETIFLGSRRPMMPTGPRRLPLPQRYWQKRPLELLGNAGCCPYGLTKTHCPLAAVY 420
DB 361 VETIFLGSRRPMMPTGPRRLPLPQRYWQKRPLELLGNAGCCPYGLTKTHCPLAAVY 420
QY 421 PAAGVCAAREKPOGSAAPBEEDTDPRRLVOLLQSHSPWQYGFVPAACLRRLVPEGLWS 480
DB 421 PAAGVCAAREKPOGSAAPBEEDTDPRRLVOLLQSHSPWQYGFVPAACLRRLVPEGLWS 480
QY 481 RHNERRFLRNTKFTISLGKAKLSLOELTWKMSVRCAMLRSPGVCVPAASHRLREEL 540
DB 481 RHNERRFLRNTKFTISLGKAKLSLOELTWKMSVRCAMLRSPGVCVPAASHRLREEL 540
QY 541 LAKFLHMLSVYVELLSFFVYTTTFOKNRLFFRPSVWSYLOSGIGRQHLKRYOLRE 600
DB 541 LAKFLHMLSVYVELLSFFVYTTTFOKNRLFFRPSVWSYLOSGIGRQHLKRYOLRE 600
QY 601 LSEAEVROHREARPAITLSRLFPKPDGLRPVNMNDYVGARTPPREKARELTSRVKA 660
DB 601 LSEAEVROHREARPAITLSRLFPKPDGLRPVNMNDYVGARTPPREKARELTSRVKA 660
QY 661 LFSVLYNERARRPDLGLASVLDGDIHRARMTFLSVRAQDPPELFPVKVDTGAYDTI 720
DB 661 LFSVLYNERARRPDLGLASVLDGDIHRARMTFLSVRAQDPPELFPVKVDTGAYDTI 720
QY 721 PQRPLTVIASIIPQNTYCVRRYAVYQKAAHGVKAPKSHSTLTLDQPMRQFVAHL 780
DB 721 PQRPLTVIASIIPQNTYCVRRYAVYQKAAHGVKAPKSHSTLTLDQPMRQFVAHL 780
QY 781 QETSPLDAVAVIQSSSLNASSGLFDFVLFPMCHAVIRKGSYVQCGIPOGSILSTL 840
DB 781 QETSPLDAVAVIQSSSLNASSGLFDFVLFPMCHAVIRKGSYVQCGIPOGSILSTL 840
QY 841 LCSCICYDMENKLPAGIRPGLLRVLDPLVLTPLHTAKTLRLTVNGVPEYGCVM 900
DB 841 LCSCICYDMENKLPAGIRPGLLRVLDPLVLTPLHTAKTLRLTVNGVPEYGCVM 900
QY 901 RKTVMNPFVDEALGFAFQMPAHGFPWCGLLTRTEVQSDVSSYARTSIRASVTF 960
DB 901 RKTVMNPFVDEALGFAFQMPAHGFPWCGLLTRTEVQSDVSSYARTSIRASVTF 960
QY 961 NRGFKAGNNRRKLPGLVRLKCHSLPLDQVNSLQTVCTNIIYKILLQAVRFAVYOLP 1020
DB 961 NRGFKAGNNRRKLPGLVRLKCHSLPLDQVNSLQTVCTNIIYKILLQAVRFAVYOLP 1020
QY 1021 FHOQVMKNPFPLRVISDTASLCYSILKAKNAGMSLGAGGAAPLSEBAVOMLCHQAPFL 1080
DB 1021 FHOQVMKNPFPLRVISDTASLCYSILKAKNAGMSLGAGGAAPLSEBAVOMLCHQAPFL 1080
QY 1081 KLTSHRVTYVPLLSJRTAQTQSRKLPGLTTLTALEAANPALPSPDKTILD 1132
DB 1081 KLTSHRVTYVPLLSJRTAQTQSRKLPGLTTLTALEAANPALPSPDKTILD 1132
RESULT 14
ABR42384
ID ABR42384 standard; protein; 1132 AA.
XX
XX ABR42384;
XX
XX 11-AUG-2003 (first entry)
XX
XX Human telomerase reverse transcriptase.
XX
XX DE Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
XX KW short interfering RNA; siRNA; cancer; tumor; cytosolic; contraceptive;
XX KW immunosuppressive; antifertility; fungicide; antiparasitic;
XX KW antiinflammatory; human; gene therapy.
XX
XX OS Homo sapiens.
XX

PN WO2003035667-A2.
 XX
 PD 01-MAY-2003.
 XX
 PE 16-OCT-2002; 2002MO-US033065.
 XX
 PR 22-OCT-2001; 2001US-0345326P.
 PR 20-FEB-2002; 2002US-0359196P.
 PR 22-MAY-2002; 2002US-0383195P.
 XX
 PA (UVRP) UNIV ROCHESTER.
 XX
 PI Rowley PT.
 XX
 DR WPI; 2003-403336/38.
 DR N-PSDB; ACCS8039.
 XX
 PT Novel double-stranded short interfering RNA having sense and antisense
 PT nucleic acids which are complementary to each other and to target nucleic
 PT acid e.g., telomerase RNA or mRNA encoding telomerase reverse
 PT transcriptase.
 PT
 XX
 PS Disclosure; Fig 4; 37pp; English.
 XX
 CC The present sequence is the protein sequence of human telomerase reverse
 CC transcriptase (TERT). The invention relates to the discovery that double-
 CC stranded interfering RNAs, such as short interfering RNAs (siRNA), which
 CC target telomerase RNA or TERT mRNA are capable of inhibiting telomerase
 CC activity. Inhibition of telomerase in cancer cells leads to telomere
 CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
 CC telomerase activity can also be used for treatment of infertility, for
 CC contraception or sterilisation, for immunosuppression, for treatment of
 CC yeast, parasite and fungal infections, and in anti-inflammatory therapies.
 CC As telomerase is active in a limited number of cell types, e.g. tumor
 CC cells, germ-line cells, certain stem cells of the haematopoietic system, T
 CC and B cells, sun-damaged skin, and proliferative cervix, most normal
 CC cells are not affected by telomerase RNA interference therapy
 CC
 XX
 SQ Sequence 1132 AA.
 Query Match 99.8%; Score 5952; DB 6; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPRAPRCAVSLSLRSHREVLPLATFYRRLGPGMRLVGGDPAPAFALVAQGLVCPM 60
 Db 1 MPRAPRCAVSLSLRSHREVLPLATFYRRLGPGMRLVGGDPAPAFALVAQGLVCPM 60
 QY 61 DARPAPAPSPRQVSCLEKELVAVLQRLCERGANVLAFGFALLDGAAGGPPAFTTSVR 120
 Db 61 DARPAPAPSPRQVSCLEKELVAVLQRLCERGANVLAFGFALLDGAAGGPPAFTTSVR 120
 QY 121 SYLNTWTDALRGSGAGMLLRVGGDPVYVHLRLCALFLVVAHSCAYVCGPPLVQLGA 180
 Db 121 SYLNTWTDALRGSGAGMLLRVGGDPVYVHLRLCALFLVVAHSCAYVCGPPLVQLGA 180
 QY 181 ATOARPPPHASGPRRLGCEERAMNHSVNEAGVPLGLPAGARRRGSGASRLPLPKPRR 240
 Db 181 ATOARPPPHASGPRRLGCEERAMNHSVNEAGVPLGLPAGARRRGSGASRLPLPKPRR 240
 QY 241 GAABEPRTPVGGQSWAHPRGTRGSDRGFCVSPAPAPAEATLDEALGSTRSHSVG 300
 Db 241 GAABEPRTPVGGQSWAHPRGTRGSDRGFCVSPAPAPAEATLDEALGSTRSHSVG 300
 QY 301 RQHAGPSTSRPPRPMDTCCPPVYAEKHFLLYSGGDEQRLPFLLSLRLTGARRL 360
 Db 301 RQHAGPSTSRPPRPMDTCCPPVYAEKHFLLYSGGDEQRLPFLLSLRLTGARRL 360
 QY 361 VETIFLGSRPWMPGTGTRLPRLPQRYWQMRPLFELLGNHQCCEYGVLLKTHCLRAVLT 420
 Db 361 VETIFLGSRPWMPGTGTRLPRLPQRYWQMRPLFELLGNHQCCEYGVLLKTHCLRAVLT 420
 QY 421 PAAGVCAEKPGQGVAAPEEEDTDPRLVQLLRQSSPMQYGVFVACLRRLVPPGLMGS 480

Db 421 PAAGVCAEKPGQGVAAPEEEDTDPRLVQLLRQSSPMQYGVFVACLRRLVPPGLMGS 480
 QY 481 RENERPFLNRTKFKFISLGGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAEHRLEBEI 540
 Db 481 RENERPFLNRTKFKFISLGGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAEHRLEBEI 540
 QY 541 LAKFLHMLMSVYVALLSPFYVTTTQXKRLPFYRSPVWSKLSIGIRQHLKRVQIRE 600
 Db 541 LAKFLHMLMSVYVALLSPFYVTTTQXKRLPFYRSPVWSKLSIGIRQHLKRVQIRE 600
 QY 601 LSEAEVRQREARPPALITSRLRFIPKPDGLPIVMMDYVVGARFPREREKRAERLTSRYKA 660
 Db 601 LSEAEVRQREARPPALITSRLRFIPKPDGLPIVMMDYVVGARFPREREKRAERLTSRYKA 660
 QY 661 LFSVINYERARRPPGLIGASVIGLDIHRAMRTFVLRYAODPPPELYEVKVDVTGAYDTI 720
 Db 661 LFSVINYERARRPPGLIGASVIGLDIHRAMRTFVLRYAODPPPELYEVKVDVTGAYDTI 720
 QY 721 PODRLTEVYASTIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 Db 721 PODRLTEVYASTIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPLRDAVVIQSSSINEASSGLFDVFLRFMCHAAVRIRKSVYVCCGIPQGSILSTL 840
 Db 781 QETSPLRDAVVIQSSSINEASSGLFDVFLRFMCHAAVRIRKSVYVCCGIPQGSILSTL 840
 QY 841 LLSLCYGDMENTLPGAIRDDGLLELVDDPLLVTPHLTHAKTEFLTLYRGVEYGCYVNL 900
 Db 841 LLSLCYGDMENTLPGAIRDDGLLELVDDPLLVTPHLTHAKTEFLTLYRGVEYGCYVNL 900
 QY 901 RKTVMNFPVEDALAGTAFVQMPAHGLPFWCGILLDTLREYQSDYSYARTSRASYTF 960
 Db 901 RKTVMNFPVEDALAGTAFVQMPAHGLPFWCGILLDTLREYQSDYSYARTSRASYTF 960
 QY 961 NRGFAGRNMRKRLFGVRLKCHSLFLDLQVNSLQTVCTNITKILLQAYRHHACVLOLP 1020
 Db 961 NRGFAGRNMRKRLFGVRLKCHSLFLDLQVNSLQTVCTNITKILLQAYRHHACVLOLP 1020
 QY 1021 FHOQWKQPTFLRYISDTASLCYSILKXKNAGMSLGAAGAPLSEAVQWLCHQAFLL 1080
 Db 1021 FHOQWKQPTFLRYISDTASLCYSILKXKNAGMSLGAAGAPLSEAVQWLCHQAFLL 1080
 QY 1081 KLTRHRVTYVPLLSLRTAQQLSRKLPQTTLTALEAANPALPSDFKTIID 1132
 Db 1081 KLTRHRVTYVPLLSLRTAQQLSRKLPQTTLTALEAANPALPSDFKTIID 1132
 RESULT 15
 ABR42063
 ID ABR42063 standard; protein; 1132 AA.
 XX
 XX ABR42063;
 DT 28-JUL-2003 (first entry)
 XX
 XX Human telomerase reverse transcriptase.
 DE
 XX Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
 KM short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
 KM immunosuppressive; anti-infertility; fungicide; antiparasitic;
 KM anti-inflammatocty; human; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO2003034985-A2.
 XX
 PD 01-MAY-2003.
 XX
 PE 16-OCT-2002; 2002MO-US033146.
 PR 22-OCT-2001; 2001US-0345326P.
 PR 20-FEB-2002; 2002US-0359196P.
 PR

PR 22-MAY-2002; 2002US-0383195P.
 XX (UTRP) UNIV ROCHESTER.
 XX Rowley PT;
 XX WPI: 2003-403289/38.
 DR N-PSDB; ACC57552.
 PT Novel nucleic acid encoding or comprising interfering RNAs which target
 PT telomerase RNA, useful for inhibiting telomerase activity for treating
 PT cancer, infertility and disorders of the immune system.
 XX
 PS Disclosure; Fig 4; 52pp; English.
 CC The present sequence is that of human telomerase reverse transcriptase
 CC (TERT). The invention relates to the discovery that double-stranded
 CC interfering RNAs, such as short interfering RNAs (siRNAs), which target
 CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
 CC activity. Inhibition of telomerase in cancer cells leads to telomere
 CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
 CC telomerase activity can also be used for treatment of infertility, for
 CC contraception or sterilisation, for immunosuppression, for treatment of
 CC yeast, parasite and fungal infections, and in anti-inflammatory therapies.
 CC As telomerase is active in a limited number of cell types, e.g. tumour
 CC cells, germ-line cells, certain stem cells of the haematopoietic system, T
 CC and B cells, sun-damaged skin, and proliferative cervix, most normal
 CC cells are not affected by telomerase RNA interference therapy
 XX
 SQ Sequence 1132 AA:
 Query Match 99.8%; Score 5952; DB 6; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPBAPCRARSLRSHYREVLPLATFVRRLPGQWRLVORDPAPFALVACVYCW 60
 DB 1 MPBAPCRARSLRSHYREVLPLATFVRRLPGQWRLVORDPAPFALVACVYCW 60
 QY 61 DARPAPASFRQVSLKELVARVLQRLCERGAKNVLAFFALLDGAAGPPEAFTTSYR 120
 DB 61 DARPAPASFRQVSLKELVARVLQRLCERGAKNVLAFFALLDGAAGPPEAFTTSYR 120
 QY 121 SYLPNTVTALRSGAGMLLRVGDVTVHLLARCALVVAFCAYVCGPPLYOGA 180
 DB 121 SYLPNTVTALRSGAGMLLRVGDVTVHLLARCALVVAFCAYVCGPPLYOGA 180
 QY 181 ATQARPPPHASGPRRLGGERAMNHSVRAGVPLGLPAGARRGGSASRSLPLPKRPR 240
 DB 181 ATQARPPPHASGPRRLGGERAMNHSVRAGVPLGLPAGARRGGSASRSLPLPKRPR 240
 QY 241 GAAPBEPRTPVGGGVAHPGRTGPDGFCVVSPPAPAEATSLGALSGTRHSHPSVG 300
 DB 241 GAAPBEPRTPVGGGVAHPGRTGPDGFCVVSPPAPAEATSLGALSGTRHSHPSVG 300
 QY 301 ROHHAGPPTSRPRPMDTPCPPVVAETGFLYSGDKQLRPSFLLSLRPSLTGARRL 360
 DB 301 ROHHAGPPTSRPRPMDTPCPPVVAETGFLYSGDKQLRPSFLLSLRPSLTGARRL 360
 QY 361 VETIFLGSRPMWGPTRRLPLRPLRYWQWRPLFELIGNHAQCPYVLKTHCPRAAVT 420
 DB 361 VETIFLGSRPMWGPTRRLPLRPLRYWQWRPLFELIGNHAQCPYVLKTHCPRAAVT 420
 QY 421 PAAGVAREKPGQSVAAPEEDTPRRVLQRLRQSSPMQYVGFRACLRLRVPGLWGS 480
 DB 421 PAAGVAREKPGQSVAAPEEDTPRRVLQRLRQSSPMQYVGFRACLRLRVPGLWGS 480
 QY 481 RHNERFLNRTKFTLSLGHAKLSLOELTKMSVDCAMLRSPGVCPAAEHRLREI 540
 DB 481 RHNERFLNRTKFTLSLGHAKLSLOELTKMSVDCAMLRSPGVCPAAEHRLREI 540
 QY 541 LAKFLHMLSVYVELLSFFVYVTTTFOKNTLFFRPSVSKLSIGIRQLKRVQURE 600
 DB 541 LAKFLHMLSVYVELLSFFVYVTTTFOKNTLFFRPSVSKLSIGIRQLKRVQURE 600

DB 541 LAKFLHMLSVYVELLSFFVYVTTTFOKNTLFFRPSVSKLSIGIRQLKRVQURE 600
 QY 601 LSEAEVROHREARPALITSLRFLPKPDGLRPIVNDYVVGARTFREREKAERLTSRYKA 660
 DB 601 LSEAEVROHREARPALITSLRFLPKPDGLRPIVNDYVVGARTFREREKAERLTSRYKA 660
 QY 661 LFSVANTERARPGGLLASVGLDIIHRAMTFLRLRACDPPELYFVAVDVTGAADTI 720
 DB 661 LFSVANTERARPGGLLASVGLDIIHRAMTFLRLRACDPPELYFVAVDVTGAADTI 720
 QY 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 DB 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSELDVAVIEOSSSLNEASGLPDVPLRFMCHAVRIRGKSVYOCOGIPGGSILSTL 840
 DB 781 QETSELDVAVIEOSSSLNEASGLPDVPLRFMCHAVRIRGKSVYOCOGIPGGSILSTL 840
 QY 841 LCSLCYGMENKLPAGIRBDGLLRLVDPLVPLTHAKTFLRLTVRGVPEYGVNVL 900
 DB 841 LCSLCYGMENKLPAGIRBDGLLRLVDPLVPLTHAKTFLRLTVRGVPEYGVNVL 900
 QY 901 RKTVMNPPVEDALGTAFAVQMPAHGLFPCGGLLDRTLEVSDVSSYARTSIRASLTF 960
 DB 901 RKTVMNPPVEDALGTAFAVQMPAHGLFPCGGLLDRTLEVSDVSSYARTSIRASLTF 960
 QY 961 NRGKAGRNMRKLPGLRLKCHSLFLDLQVNSIQVCTNIYKILLQAYRFACVLOLP 1020
 DB 961 NRGKAGRNMRKLPGLRLKCHSLFLDLQVNSIQVCTNIYKILLQAYRFACVLOLP 1020
 QY 1021 FHQGVKNPFFLRVISTDASLCYSIIKANAGKSGAKGAAPLPSEAVQWLCHQAFUL 1080
 DB 1021 FHQGVKNPFFLRVISTDASLCYSIIKANAGKSGAKGAAPLPSEAVQWLCHQAFUL 1080
 QY 1081 KLTHRTVTPILGSLTFAOTLSRKLPGTTLTALLEANPAPSPFKITLD 1132
 DB 1081 KLTHRTVTPILGSLTFAOTLSRKLPGTTLTALLEANPAPSPFKITLD 1132
 RESULT 16
 ID ABB56676 standard; protein; 1132 AA.
 XX ABB56676;
 XX 25-MAR-2003 (first entry)
 DE Human telomerase reverse transcriptase protein SEQ ID NO:2.
 XX Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;
 KM vulnereary; anticulcer; epithelial cell migration promoter; wound;
 KM epithelial cell; keratinocyte; epidermal; mucosal.
 OS Homo sapiens.
 XX MO200291999-A2.
 XX 21-NOV-2002.
 PD 03-MAY-2002; 2002MO-US014867.
 PF 09-MAY-2001; 2001US-0289903P.
 PR (GERO-) GERON CORP.
 PA Jiang X, Chiu C, Harley CB;
 PI WPI: 2003-120591/11.
 DR N-PSDB; AB222474.
 XX Composition for treating wounds and enhancing epithelialization of a skin
 PT surface, comprises vector encoding telomerase reverse transcriptase or

PT telomerized epithelial cells on a microparticle or a matrix.
 XX
 PS Disclosure; Page 32; 68pp; English.

XX
 CC The present invention describes a pharmaceutical composition (I) comprising a vector encoding telomerase reverse transcriptase (TERT) in an excipient or device, or comprises telomerized epithelial cells on a microparticle or a matrix suitable for topical administration or administration to a wound site. (I) has a vulnereary and anticulcer activities and can be used to promote epithelial cell migration. (I) is useful for treating a wound and enhancing epithelialization of a skin surface. The wound is especially a skin wound including acute lesion such as traumatic lesion, burn, or surgical incision, chronic lesion such as chronic venous ulcer, diabetic ulcer or compression ulcer and the wound is further monitored for closure. The telomerase activity or TERT expression is increased in epithelial cells at the site of treatment and also in fibroblasts or endothelial cells at the site of treatment. The epithelial cells are especially keratinocytes. A polynucleotide encoding TERT is useful for the preparation of a medicament for treatment of a wound or an epithelial surface in a human or animal. An epithelial cell with increased telomerase activity or increased expression of TERT is useful for preparation of a medicament for the treatment of a wound in a human or animal. (I) is also useful for treating wounds of other epithelial surfaces including mucosal surfaces such as bronchus, mouth, nose, oesophagus, stomach, or intestine. The present sequence represents human TERT (hTERT), which is given in the exemplification of the present invention. hTERT is located to chromosome 5

XX
 SO Sequence 1132 AA:

Query Match 99.8%; Score 5952; DB 6; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCAVAVSLIRSHYREYLPATFVRRLGPGQWMLVORGDPAPRALVAOCLVCPV 60
 DB 1 MPRAPRCAVAVSLIRSHYREYLPATFVRRLGPGQWMLVORGDPAPRALVAOCLVCPV 60
 QY 61 DARPAPAPSFQVYSCUKELVAVYLRQLCERGANVLAFAFALLDAGRGSPPAFTTSVR 120
 DB 61 DARPAPAPSFQVYSCUKELVAVYLRQLCERGANVLAFAFALLDAGRGSPPAFTTSVR 120
 QY 121 SYLPNTVTDALRGSGAGLLRRYGDVIVHLLARCLFVLVAPSCAYVCGPPLVQLGA 180
 DB 121 SYLPNTVTDALRGSGAGLLRRYGDVIVHLLARCLFVLVAPSCAYVCGPPLVQLGA 180
 QY 181 ATQARPPPHASGPRRLRGGERAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKPRR 240
 DB 181 ATQARPPPHASGPRRLRGGERAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKPRR 240
 QY 241 GAAPERPRTVYGQGSMAHPGKTRGSPDRGFCVSPAPAPAEATSLLEALSGTRSHSPV 300
 DB 241 GAAPERPRTVYGQGSMAHPGKTRGSPDRGFCVSPAPAPAEATSLLEALSGTRSHSPV 300
 QY 241 GAAPERPRTVYGQGSMAHPGKTRGSPDRGFCVSPAPAPAEATSLLEALSGTRSHSPV 300
 DB 241 GAAPERPRTVYGQGSMAHPGKTRGSPDRGFCVSPAPAPAEATSLLEALSGTRSHSPV 300
 QY 301 ROHHAGPSTGRPRPMDTPCPFYAATKHLVSSGDKQOLRPSFLLSLRPSLTGARRL 360
 DB 301 ROHHAGPSTGRPRPMDTPCPFYAATKHLVSSGDKQOLRPSFLLSLRPSLTGARRL 360
 QY 361 VETIFIGSRPWPMPGTPLRLPLPORYWQMRPLFELLIGNHAOCFYVLLKTHCPRAAVT 420
 DB 361 VETIFIGSRPWPMPGTPLRLPLPORYWQMRPLFELLIGNHAOCFYVLLKTHCPRAAVT 420
 QY 421 PAAVCARERKQGSVAAPBEEDTDPRRLVOLLRSHSPWQYGVYACLRILVPGMG 480
 DB 421 PAAVCARERKQGSVAAPBEEDTDPRRLVOLLRSHSPWQYGVYACLRILVPGMG 480
 QY 421 PAAVCARERKQGSVAAPBEEDTDPRRLVOLLRSHSPWQYGVYACLRILVPGMG 480
 DB 421 PAAVCARERKQGSVAAPBEEDTDPRRLVOLLRSHSPWQYGVYACLRILVPGMG 480
 QY 481 RHNERRRFRLNTKFTSLGKHAHLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
 DB 481 RHNERRRFRLNTKFTSLGKHAHLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
 QY 541 LAKPLHMTMSYVVVLLRSFYVTTTTOCKRRLFFYRSVWSKIOSIGIOHKLRYOLRE 600
 DB 541 LAKPLHMTMSYVVVLLRSFYVTTTTOCKRRLFFYRSVWSKIOSIGIOHKLRYOLRE 600
 QY 600 LAKPLHMTMSYVVVLLRSFYVTTTTOCKRRLFFYRSVWSKIOSIGIOHKLRYOLRE 600
 DB 600 LAKPLHMTMSYVVVLLRSFYVTTTTOCKRRLFFYRSVWSKIOSIGIOHKLRYOLRE 600

QY 601 LSEAFVROHREARPALTLSTRLFIPKPDGLRPIVNMQYVGAFTFRREKRAERLTSRYKA 660
 DB 601 LSEAFVROHREARPALTLSTRLFIPKPDGLRPIVNMQYVGAFTFRREKRAERLTSRYKA 660
 QY 661 LFSVINYERARPPGLIGASVILGDDIHRAMTFVILRVRAOQPPBELYFKVDYGAVDTI 720
 DB 661 LFSVINYERARPPGLIGASVILGDDIHRAMTFVILRVRAOQPPBELYFKVDYGAVDTI 720
 QY 721 PODRLTEVIASIKRONTYCVRRYAVVQKAAHGRKAFKSHVSTLTDLQYMFQVAHL 780
 DB 721 PODRLTEVIASIKRONTYCVRRYAVVQKAAHGRKAFKSHVSTLTDLQYMFQVAHL 780
 QY 781 QETSPRLDAVYIEQSSSLNEASSGLFDVFLRFMCHAVRIRKSGYVCCGIPQGSILSTL 840
 DB 781 QETSPRLDAVYIEQSSSLNEASSGLFDVFLRFMCHAVRIRKSGYVCCGIPQGSILSTL 840
 QY 841 LCSLCYGMENKLPAGIRDDGLLRVDDPILVPHLTHAKTFRLTVRGVDEYGVNVL 900
 DB 841 LCSLCYGMENKLPAGIRDDGLLRVDDPILVPHLTHAKTFRLTVRGVDEYGVNVL 900
 QY 901 RKTIVNFVEDEALOGTAFVQMPAHGLFPWCGLLDTRTEVQSDYSYARTSIRASVTF 960
 DB 901 RKTIVNFVEDEALOGTAFVQMPAHGLFPWCGLLDTRTEVQSDYSYARTSIRASVTF 960
 QY 961 NRGFPAAGNMRRKLFVILRLKCHSLFDLOVNSLOTCTNITYKILLQAYRFAVCVQLP 1020
 DB 961 NRGFPAAGNMRRKLFVILRLKCHSLFDLOVNSLOTCTNITYKILLQAYRFAVCVQLP 1020
 QY 1021 FHOQVWKQPTFLKXISDTASLCYSILKAKNAGMSLGAKGAGPLPSBAVQMLCHQAFLL 1080
 DB 1021 FHOQVWKQPTFLKXISDTASLCYSILKAKNAGMSLGAKGAGPLPSBAVQMLCHQAFLL 1080
 QY 1081 KLTRHRTVYVPLIGSLRTAQOLSRKLPQTTLTALAANPALPSDFETIID 1132
 DB 1081 KLTRHRTVYVPLIGSLRTAQOLSRKLPQTTLTALAANPALPSDFETIID 1132

RESULT 17
 ABR58045
 ID ABR58045 standard; protein; 1132 AA.
 AC ABR58045;
 DT 29-AUG-2003 (first entry)
 DE Human telomerase reverse transcriptase.
 EE Enzyme; human; telomerase reverse transcriptase; adipogenic capacity;
 KW primary preadipocyte cell; adipogenesis; obesity; adipocytokine;
 OS anorectic; adiponectin; insulin.
 OS Homo sapiens.
 PN WO2003031640-A2.
 PD 17-APR-2003.
 PF 07-OCT-2002; 2002WO-US031635.
 PR 06-OCT-2001; 2001US-0327650P.
 PR 06-OCT-2001; 2001US-0327651P.
 PA (BOST-) BOSTON MEDICAL CENT CORP.
 PI Kirkland J, Tchekonia T;
 DR MPI; 2003-421278/39.
 DR N-PSDB; ACC44482.
 PT New primary preadipocyte strain expressing telomerase reverse transcriptase, useful in research applications, screening assays, clinical applications, and in the administration of therapeutic agents.

particularly for obesity.

XX Disclosure; Page 13; 53pp; English.

XX The invention relates to the generation of primary preadipocyte cell

CC strains that express telomerase reverse transcriptase (TERT, the

CC catalytic subunit of telomerase), and maintain and/or enhance replicative

CC potential and maintain adipogenic capacity of the cell. This sequence

CC represents the TERT protein. The cell strain can be used in research to

CC study all aspect of adipogenesis, especially in relation to researching

CC treatments for e.g. obesity. The cell can also be used to identify

CC adipogenesis modulators for use as therapeutic agents such as hormones,

CC growth factors, cytokines, enzymes, cholesterol binding proteins,

CC cholesterol removing proteins or their combinations. Alternatively, the

CC therapeutic agent may be an adipocytokine, preferably adiponectin, or

CC insulin

XX

XX Sequence 1132 AA;

Query Match. 99.8%; Score 5952; DB 6; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAAPCRVRSLSLRSHREVLPLATFVRSLGPGKRLVQGRDPAFAFALVQCLVCPM 60

Db 1 MPRAAPCRVRSLSLRSHREVLPLATFVRSLGPGKRLVQGRDPAFAFALVQCLVCPM 60

QY 61 DAPPPAPAPSFROVSCLELVARVLQRLCERGAKNVLAFGALLDAGRGPEAFTTSVR 120

Db 61 DAPPPAPAPSFROVSCLELVARVLQRLCERGAKNVLAFGALLDAGRGPEAFTTSVR 120

QY 121 SYLPTVTVALRSGGAWGILLRRVGDVYLHLLARCALFVLAAPCAVQVCPPLIYQGA 180

Db 121 SYLPTVTVALRSGGAWGILLRRVGDVYLHLLARCALFVLAAPCAVQVCPPLIYQGA 180

QY 181 ATQARPPHASPGRRLGGERAMNSVREAGVPLGLPAGARRGSGASRSILPLKPRR 240

Db 181 ATQARPPHASPGRRLGGERAMNSVREAGVPLGLPAGARRGSGASRSILPLKPRR 240

QY 241 GAAPBERPVPVGGSAHAPGRTGRGSDRGFCVSPAPPAEATSLGALSGTRHSPVG 300

Db 241 GAAPBERPVPVGGSAHAPGRTGRGSDRGFCVSPAPPAEATSLGALSGTRHSPVG 300

QY 301 ROHHAGPSTSRPPRMWDTCPFPVVAETGHLFYSDDXELPAPSLSLRPSLTGARRL 360

Db 301 ROHHAGPSTSRPPRMWDTCPFPVVAETGHLFYSDDXELPAPSLSLRPSLTGARRL 360

QY 361 VETIFLGSRRPMPGTPRLPLPQRYWQNRPLFELLGNAQCPYVZLKTCHPLRAAVT 420

Db 361 VETIFLGSRRPMPGTPRLPLPQRYWQNRPLFELLGNAQCPYVZLKTCHPLRAAVT 420

QY 421 PAAGVABRKPQGVAAPEEDTDPRLVQLRQSSPMQVYGFRACTRLRVPGLMGS 480

Db 421 PAAGVABRKPQGVAAPEEDTDPRLVQLRQSSPMQVYGFRACTRLRVPGLMGS 480

QY 481 RHNERFLNRTKKFSLGKAKLSLOELTKMSVBDCAWLRSPGVGCPAAEHLREBI 540

Db 481 RHNERFLNRTKKFSLGKAKLSLOELTKMSVBDCAWLRSPGVGCPAAEHLREBI 540

QY 541 LAKFLHMLSVYVVELRSFFVYETTPQKRLFFYRPSVSKLSIGIRQHLKRVQRE 600

Db 541 LAKFLHMLSVYVVELRSFFVYETTPQKRLFFYRPSVSKLSIGIRQHLKRVQRE 600

QY 601 LSEAEVRQREARPALTLRLRFIPKPDGLRPIVMDVVGARTRREKRAERLTSRYKA 660

Db 601 LSEAEVRQREARPALTLRLRFIPKPDGLRPIVMDVVGARTRREKRAERLTSRYKA 660

QY 661 LRSVLYNEARPPGLIGASVGLDIDIRAMRTFVLRPAODPPRLYVAVDVGADYTI 720

Db 661 LRSVLYNEARPPGLIGASVGLDIDIRAMRTFVLRPAODPPRLYVAVDVGADYTI 720

QY 721 PDDRLTEVIASTIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780

Db 721 PDDRLTEVIASTIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780

Db 721 PDDRLTEVIASTIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780

QY 781 QETSLPDAVITEOSSSLNASSGLPDLFLRPMCHAVRIRGKSYVQCGIIPGGSILSTL 840

Db 781 QETSLPDAVITEOSSSLNASSGLPDLFLRPMCHAVRIRGKSYVQCGIIPGGSILSTL 840

QY 841 LCSLCYDMDENKLPAGIRRDGLLRVDLTLVPHLTHAKTFLRLVRCVPEYGVVNL 900

Db 841 LCSLCYDMDENKLPAGIRRDGLLRVDLTLVPHLTHAKTFLRLVRCVPEYGVVNL 900

QY 901 RKTVMNPFVDEALGGAFAVQMPAHGIFPWCGLLDTRELVSDYSVARTSRASVTF 960

Db 901 RKTVMNPFVDEALGGAFAVQMPAHGIFPWCGLLDTRELVSDYSVARTSRASVTF 960

QY 961 NRGFKARNRKRLFGVLRKCHSLPDLQVNSLQTCVNIYKILLQVRFPAVYLQLP 1020

Db 961 NRGFKARNRKRLFGVLRKCHSLPDLQVNSLQTCVNIYKILLQVRFPAVYLQLP 1020

QY 1021 FHQGVKNPFFPLRVISDTSLCYSLIKAVAGMSIGANGAGPLPSEAVQMLCHQAFLL 1080

Db 1021 FHQGVKNPFFPLRVISDTSLCYSLIKAVAGMSIGANGAGPLPSEAVQMLCHQAFLL 1080

QY 1081 KLTRHRTVYPLGSLRTAQTOLSRKLPPTTLTALAAANPALPSPFKTILD 1132

Db 1081 KLTRHRTVYPLGSLRTAQTOLSRKLPPTTLTALAAANPALPSPFKTILD 1132

RESULT 18

ID ADD21420

AD ADD21420 standard; protein; 1132 AA.

XX

AC ADD21420;

XX

DT 15-JAN-2004 (first entry)

XX

XX Human TERT protein related to continual cell growth.

XX

KW continual growth; cultured cell; cyclin dependent kinase; cdk4; cdk2;

KW cdk6; activating mutation; cell growth; cell division; cell cycle;

KW cancer-causing agent; continual growth-induced cell; enzyme; TERT;

KW telomerase; human.

XX

OS Homo sapiens.

XX

PN W02003044169-A2.

PD 30-MAY-2003.

XX

PF 15-NOV-2002; 2002MO-US036729.

XX

PR 15-NOV-2001; 2001US-0334760P.

XX

PA (ITEM) UNIV TEMPLE.

PI Reddy PE, Rane SG, Mettus RV;

XX

PI WPI; 2003-449813/42.

XX

PT A composition for reversibly inducing continual growth in normal cells

PT comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or

PT its active fragment, derivative, homolog or analog, having an activating

PT mutation.

XX

PS Claim 16; Page 135-138; 77pp; English.

XX

CC This invention relates to a novel composition for inducing a reversible

CC state of a continual growth in cultured cells and comprises at least one

CC compound comprising a cyclin dependent kinase (cdk)4, cdk2 or cdk6

CC protein having an activating mutation. Growth and division of living

CC cells involve a regular series of events and processes that comprise the

CC cell cycle. Cyclin dependent kinases cdk2, cdk4 and cdk6 are involved in

CC the control of G1, the point at which cells irreversibly commit to DNA

CC synthesis and thus enter the cell cycle. The invention is useful in

CC reversibly inducing continual growth in normal cells and may allow the
 CC screening of cancer-causing agents with the continual growth-induced
 CC cells. The present sequence is that of the human TERT protein, the
 CC catalytic subunit of telomerase, related to the invention. Note: Due to
 CC an error in the specification or sequence listing, the Seq ID numbers
 CC given in the disclosure do not correspond to those given in the sequence
 CC listing. It is therefore unclear which Seq ID number corresponds to which
 CC sequence and exactly which sequence is being claimed.

XX Sequence 1132 AA;

Query Match 99.8%; Score 5952; DB 7; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLRSHYREVLPLATFVRRLGPGQRLVORGDPAPAFALVACLVCPWM 60
 Db 1 MPAPRCRAVRSLRSHYREVLPLATFVRRLGPGQRLVORGDPAPAFALVACLVCPWM 60
 QY 61 DARPAPAPSPROVSCIKELVAVLQRLCERGAKNVLAFGFALLDAGRGPPAFTSVR 120
 Db 61 DARPAPAPSPROVSCIKELVAVLQRLCERGAKNVLAFGFALLDAGRGPPAFTSVR 120
 QY 121 SYTPNTVTDALRSGSGAMGLLRVGDVYLHLLARCLFVLVAPSCAYOVCGPPLYQLGA 180
 Db 121 SYTPNTVTDALRSGSGAMGLLRVGDVYLHLLARCLFVLVAPSCAYOVCGPPLYQLGA 180
 QY 181 ATQARPPHAGSPRRAGCERAMNHSVREAGVPLGAPAGARRGGSASHSLPLKRRPR 240
 Db 181 ATQARPPHAGSPRRAGCERAMNHSVREAGVPLGAPAGARRGGSASHSLPLKRRPR 240
 QY 241 GAAPERPRTVGGGSAWHPRTGPGSRGCVVSPAPAEALSLRGALSGTHSPSVG 300
 Db 241 GAAPERPRTVGGGSAWHPRTGPGSRGCVVSPAPAEALSLRGALSGTHSPSVG 300
 QY 301 ROHHAGPSTSRPRPMDPCPPYATETKAFVLSGGKEQLRPSFLLSLRPLTGARRL 360
 Db 301 ROHHAGPSTSRPRPMDPCPPYATETKAFVLSGGKEQLRPSFLLSLRPLTGARRL 360
 QY 361 VETIFLGSRPWPMPGTPRRLLPRLPQRYWQMRPLFELIIGNAQCPRYVLLKTHCPLEAAT 420
 Db 361 VETIFLGSRPWPMPGTPRRLLPRLPQRYWQMRPLFELIIGNAQCPRYVLLKTHCPLEAAT 420
 QY 421 PAAGVCAERKPGQSVAPBEEDTDPRRLVQLLRHSSPMQVYGVRACLRLVPPGLMGS 480
 Db 421 PAAGVCAERKPGQSVAPBEEDTDPRRLVQLLRHSSPMQVYGVRACLRLVPPGLMGS 480
 QY 481 RHNERRLRNTKRFISLGKHAKLJLQELTWKMSVRCAMLRSPGVGCVPAAERHRLBEI 540
 Db 481 RHNERRLRNTKRFISLGKHAKLJLQELTWKMSVRCAMLRSPGVGCVPAAERHRLBEI 540
 QY 541 LAKFLHMLSVYVVELLRSPFYVTTETTFQKNRLFFRPSWSKLSQSIGIQLKRYQRE 600
 Db 541 LAKFLHMLSVYVVELLRSPFYVTTETTFQKNRLFFRPSWSKLSQSIGIQLKRYQRE 600
 QY 601 LSEAEVCHREARALTSRLRFIPKPDGRLPIYNNVYVGAARFRREKAEARLTSVKA 660
 Db 601 LSEAEVCHREARALTSRLRFIPKPDGRLPIYNNVYVGAARFRREKAEARLTSVKA 660
 QY 661 LFSVYNERARPGILGASVGLDDIHRAMTFVLVRAQDPPELYFVKVDTGAYDTI 720
 Db 661 LFSVYNERARPGILGASVGLDDIHRAMTFVLVRAQDPPELYFVKVDTGAYDTI 720
 QY 721 PODLTETIASIIRKONTYCVRRAYVOKAHGVRKAFKSHVSTLIDLPYKQFPAHL 780
 Db 721 PODLTETIASIIRKONTYCVRRAYVOKAHGVRKAFKSHVSTLIDLPYKQFPAHL 780
 QY 781 QETSPRLDAVYIEOSSLINEASSGLFDVFLRFMCHAVAIRKGSYVOCQIGIPQSIISTL 840
 Db 781 QETSPRLDAVYIEOSSLINEASSGLFDVFLRFMCHAVAIRKGSYVOCQIGIPQSIISTL 840
 QY 841 LCSLCYGMENKLPAGIRDDGLLRVNDPFLVPHLTHAKTFLRLTVRGVPEYGCYVNL 900

Db 841 LCSLCYGMENKLPAGIRDDGLLRVNDPFLVPHLTHAKTFLRLTVRGVPEYGCYVNL 900
 QY 901 RKTIVNFEVEDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVSQSYASRTASVTF 960
 Db 901 RKTIVNFEVEDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVSQSYASRTASVTF 960
 QY 961 NRGFGAGNNRRKIFGVRLKCHSLFDLDVNSLQYCTNINIKYKLLQAVRFAVCVQLP 1020
 Db 961 NRGFGAGNNRRKIFGVRLKCHSLFDLDVNSLQYCTNINIKYKLLQAVRFAVCVQLP 1020
 QY 1021 FHOQWKNPTEFLRVISPTASLCYSILKAKAGMSLAKGAGPLPEBAVQMLCHOAFLL 1080
 Db 1021 FHOQWKNPTEFLRVISPTASLCYSILKAKAGMSLAKGAGPLPEBAVQMLCHOAFLL 1080
 QY 1081 KLTRRRTVYVPLGSLRTAQOLSRKLPGTTTLALBAANPALPSDFKTIID 1132
 Db 1081 KLTRRRTVYVPLGSLRTAQOLSRKLPGTTTLALBAANPALPSDFKTIID 1132
 Db 1081 KLTRRRTVYVPLGSLRTAQOLSRKLPGTTTLALBAANPALPSDFKTIID 1132
 RESULT 19
 ADH72743
 ID ADH72743 standard; protein, 1132 AA.
 XX
 AC ADH72743;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human protein of the invention SEQ ID NO:19.
 XX
 KW stem cell; cardiatic; hepatotropic; nephrotropic; cytosolic; neotropic;
 KW neoprotective; antiarthritic; antidiabetic; antiarteriosclerotic;
 KW heart failure; leukaemia; neurodegenerative disease; diabetes;
 KW arteriosclerosis; skeletal muscle; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003027281-A2.
 XX
 PD 03-APR-2003.
 XX
 PF 20-SEP-2002; 2002WO-TP009702.
 XX
 PR 20-SEP-2001; 2001JP-00286332.
 XX
 PR 09-MAY-2002; 2002JP-00133575.
 XX
 PA (KYOM) KYOMA HAKKO KOGYO KK.
 PA (TAMA/) TAMA T.
 PA (ANDO/) ANDO K.
 PI Tamaki T, Ando K, Akatsuka A, Nakamura Y, Hotta T, Sakurada K;
 XX
 DR WPI; 2003-371925/35.
 XX
 PT Pluripotent stem cells originating in skeletal muscle interstitial
 PT tissue, useful in drugs for regenerating tissues and cells e.g. in
 PT treating heart failure, leukaemia, neurodegenerative diseases, and
 PT diabetes.
 XX
 PS Disclosure; SEQ ID NO 19; 29pp; Japanese.
 XX
 CC The invention relates to novel pluripotent stem cells originating from a
 CC skeletal muscle interstitial tissue. A cell of the invention has
 CC cardiatic, hepatotropic, nephrotropic, cytosolic, antidiabetic,
 CC neoprotective, antiarthritic, antidiabetic, and antiarteriosclerotic
 CC activity. The cells are useful in drugs for regenerating tissues and
 CC cells e.g. in treating heart failure, leukaemia, neurodegenerative
 CC diseases, diabetes and arteriosclerosis. The pluripotent stem cells were
 CC isolated from rat skeletal muscles after analysis of the various
 CC components by culturing and staining, as well as by other biochemical
 CC analysis. The present sequence is used in the exemplification of the
 CC invention.
 XX
 SO Sequence 1132 AA;

Query Match 99.8%; Score 5952; DB 7; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLSHREVLPLATFVRRLQPGQRLVQGDPAFRLVAQCLVCVW 60
 DB 1 MPAPRCRAVRSLLSHREVLPLATFVRRLQPGQRLVQGDPAFRLVAQCLVCVW 60

QY 61 DAPPPAASFRQVSCIKELVARVLOQLCEBGAKNVLAFGFLLDAGAGPPEATTSVR 120
 DB 61 DAPPPAASFRQVSCIKELVARVLOQLCEBGAKNVLAFGFLLDAGAGPPEATTSVR 120

QY 121 SYLPNTVTDALRSGAGMLLRRVGDVVLHLLARCALFVLAFCAYVCCPPLYOLGA 180
 DB 121 SYLPNTVTDALRSGAGMLLRRVGDVVLHLLARCALFVLAFCAYVCCPPLYOLGA 180

QY 181 ATOARPPHAGSRRLGGERAMNSVRAGVPLGLPAGARRRGSASRLPLKRRPR 240
 DB 181 ATOARPPHAGSRRLGGERAMNSVRAGVPLGLPAGARRRGSASRLPLKRRPR 240

QY 241 GAAPERTPVGGGSAHFGRTGSPDRGFCVSPAPAEATSLGALSGTRHSPVG 300
 DB 241 GAAPERTPVGGGSAHFGRTGSPDRGFCVSPAPAEATSLGALSGTRHSPVG 300

QY 301 ROHHAAPSTSRPPRWDTPCPVVAETGHLFYSQDKQLRPSFLSLRSLTGARRL 360
 DB 301 ROHHAAPSTSRPPRWDTPCPVVAETGHLFYSQDKQLRPSFLSLRSLTGARRL 360

QY 361 VETIFGSRPMMGTRRLPRLPORWQVRPLFLELGNHACCPGVLLKTHCPRAVLT 420
 DB 361 VETIFGSRPMMGTRRLPRLPORWQVRPLFLELGNHACCPGVLLKTHCPRAVLT 420

QY 421 PAAGVAREKPOGSVAPEEDTDPRLVQLRQSSPMQVYGFVACLRLRVPEGLWS 480
 DB 421 PAAGVAREKPOGSVAPEEDTDPRLVQLRQSSPMQVYGFVACLRLRVPEGLWS 480

QY 481 RHNERFLANTKKTSLGKAALSLQELTKMSVDDCAMLRSPGVCPAAEHRLREI 540
 DB 481 RHNERFLANTKKTSLGKAALSLQELTKMSVDDCAMLRSPGVCPAAEHRLREI 540

QY 541 LAKFLHMLSVYVVELLSFFVTEETTFQKRLPFYRPSWSKLSIGIRHLKRVQRE 600
 DB 541 LAKFLHMLSVYVVELLSFFVTEETTFQKRLPFYRPSWSKLSIGIRHLKRVQRE 600

QY 601 LSEAEVRQREARPALITSLRFLFKPDGLRPIVNDYVVGARTPRRKAERLTSRYKA 660
 DB 601 LSEAEVRQREARPALITSLRFLFKPDGLRPIVNDYVVGARTPRRKAERLTSRYKA 660

QY 661 LPSVLYERARRPGLGASVGLDDIHRAWRTFVLRBAODPPPELYFKVDVTGAYDTI 720
 DB 661 LPSVLYERARRPGLGASVGLDDIHRAWRTFVLRBAODPPPELYFKVDVTGAYDTI 720

QY 721 PODRLTEVASTIKQNTYCVARVAVVOKAHGHVKAFKSHVSTLTDLPYMRQVAHL 780
 DB 721 PODRLTEVASTIKQNTYCVARVAVVOKAHGHVKAFKSHVSTLTDLPYMRQVAHL 780

QY 781 QETSPLRDAVITEOSSLINEASSGLFDVFLRPMCHAVRIGKSIYQCGIPQSSILSTL 840
 DB 781 QETSPLRDAVITEOSSLINEASSGLFDVFLRPMCHAVRIGKSIYQCGIPQSSILSTL 840

QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDPFLVTPHLLTAFTPLRTLVRGVPEXCVNL 900
 DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDPFLVTPHLLTAFTPLRTLVRGVPEXCVNL 900

QY 901 RTVYNFPEDEBALGCTAFVQMPAGLFPWCGLLDPTTLEVOGDSYATSTIRASVTF 960
 DB 901 RTVYNFPEDEBALGCTAFVQMPAGLFPWCGLLDPTTLEVOGDSYATSTIRASVTF 960

QY 961 NRGFGAGNMRRKLFGLVRLKCHSLFLDLQVNSIQTVCTNIYKLLILQAYRFAHCYQLP 1020
 DB 961 NRGFGAGNMRRKLFGLVRLKCHSLFLDLQVNSIQTVCTNIYKLLILQAYRFAHCYQLP 1020

QY 1021 FHQQWKNPFPFLVISDTASLQSYILKARNAGSLGAKGAGPLPSEAYQWICHQAFLL 1080
 DB 1021 FHQQWKNPFPFLVISDTASLQSYILKARNAGSLGAKGAGPLPSEAYQWICHQAFLL 1080

QY 1081 KLTSHRVTVYPLGLSLRTAQTOLSRKLPSTTLTALEAANPALPSPFKTILD 1132
 DB 1081 KLTSHRVTVYPLGLSLRTAQTOLSRKLPSTTLTALEAANPALPSPFKTILD 1132

RESULT 20
 ADG70114
 ID ADG70114 standard; protein: 1132 AA.
 XX
 AC ADG70114;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE hTERT protein.
 XX
 KW cytosolic; gene therapy; reverse transcriptase-inhibitor; HIV-1;
 KW human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
 KW unregulated cellular growth; cancer; tumor.
 XX
 OS Homo sapiens.
 XX
 FN MO2003095605-A2.
 XX
 PD 20-NOV-2003.
 XX
 PE 14-APR-2003; 2003MO-EP003874.
 XX
 PR 08-MAY-2002; 2002US-0378820P.
 XX
 PA (PHMA) PHARMACIA ITAL SPA.
 XX
 PI Moll J, Schmuchel A, Stouten P;
 XX
 DR WPI, 2004-012095/01.
 DR N-PSDE; ADG70113.
 XX
 PT New HIV-1 Reverse Transcriptase and human Telomerase Reverse
 PT Transcriptase proteins and nucleic acids, useful in gene therapy or for
 PT treating or preventing unregulated cellular growth, e.g. cancer cell or
 PT tumor growth.
 XX
 PS Example 1; SEQ ID NO 4; 141pp; English.
 XX
 CC The invention relates to the isolation of compounds that bind and inhibit
 CC the activity of HIV-1 reverse transcriptase (RT) or human telomerase
 CC reverse transcriptase (hTERT). The method involves determining these
 CC compounds using a HIV-1 RT/hTERT chimeric construct containing the
 CC catalytic sites of each enzyme. The nucleic acid is useful for treating
 CC or preventing unregulated cellular growth, including cancer cell and
 CC tumor growth. It is also useful in gene therapy. Compounds that inhibit
 CC telomerase activity can be used to treat cancer. The vectors of the
 CC invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
 CC express DNA which encodes HIV-RT/hTERT. This sequence corresponds to the
 CC human TERT protein.
 XX
 SQ Sequence 1132 AA;

Query Match 99.8%; Score 5952; DB 8; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLSHREVLPLATFVRRLQPGQRLVQGDPAFRLVAQCLVCVW 60
 DB 1 MPAPRCRAVRSLLSHREVLPLATFVRRLQPGQRLVQGDPAFRLVAQCLVCVW 60

QY 61 DAPPPAASFRQVSCIKELVARVLOQLCEBGAKNVLAFGFLLDAGAGPPEATTSVR 120
 DB 61 DAPPPAASFRQVSCIKELVARVLOQLCEBGAKNVLAFGFLLDAGAGPPEATTSVR 120

QY	12	SYLBNPTATDRLRGSGAWGLILRRVGDVVLNHLRACLFYLVASCAVQVCGPPLYOLGA	180
Db	121	SYLBNPTATDRLRGSGAWGLILRRVGDVVLNHLRACLFYLVASCAVQVCGPPLYOLGA	180
QY	181	ATQARPPPHASGPPRRILGCEPAMNHSVREAGVPLGLPAPGARRRGSASRSJLPLPKPRR	240
Db	181	ATQARPPPHASGPPRRILGCEPAMNHSVREAGVPLGLPAPGARRRGSASRSJLPLPKPRR	240
QY	241	GAABEPERTPVQGSMAHPGRTTRGDSRGCVSVSPAPAEAAATLEGLSSTRSHSVG	300
Db	241	GAABEPERTPVQGSMAHPGRTTRGDSRGCVSVSPAPAEAAATLEGLSSTRSHSVG	300
QY	301	ROHHAGEPSTSRPBPMDTCCPVYAETKAFLYSSGDKOULRPSFLLSLRPSLTGARL	360
Db	301	ROHHAGEPSTSRPBPMDTCCPVYAETKAFLYSSGDKOULRPSFLLSLRPSLTGARL	360
QY	361	VEITFLSRPMPGPTPRRLPELPORYOMRPLFELLGNHACQCYVLLKTHCGLBAVT	420
Db	361	VEITFLSRPMPGPTPRRLPELPORYOMRPLFELLGNHACQCYVLLKTHCGLBAVT	420
QY	421	PAAGVCAREKQGSVAABEEDTDPRRLVOLLROHSSPWQYGVFVACLRRLVPPGLWS	480
Db	421	PAAGVCAREKQGSVAABEEDTDPRRLVOLLROHSSPWQYGVFVACLRRLVPPGLWS	480
QY	481	RHNRRRLRNKKKTSIGKNAKLSLOELTWKSVRDCMILRRSGVGVCPAPAEHRLBEI	540
Db	481	RHNRRRLRNKKKTSIGKNAKLSLOELTWKSVRDCMILRRSGVGVCPAPAEHRLBEI	540
QY	541	LAKELHMLMSYVVELRSPFYVTEETTFQKRLFFYRPSVMSKLSIGIRGHLRVOLRE	600
Db	541	LAKELHMLMSYVVELRSPFYVTEETTFQKRLFFYRPSVMSKLSIGIRGHLRVOLRE	600
QY	601	LSEAEVQOHRARPAALLTSRLRFLPKRPGCAPVIMMDVAVGARTPRRKRERLISRVA	660
Db	601	LSEAEVQOHRARPAALLTSRLRFLPKRPGCAPVIMMDVAVGARTPRRKRERLISRVA	660
QY	661	LFSVLNTERARPGILGASVLGLDINHMRKTFVLRYAODRPPELYFVKADVTGAYDTI	720
Db	661	LFSVLNTERARPGILGASVLGLDINHMRKTFVLRYAODRPPELYFVKADVTGAYDTI	720
QY	721	PODLRLTEVIAIIRKQNTYCYRRAVAVOKAANGHYRKAFKSHVSTLTDLOXYMOQFAHL	780
Db	721	PODLRLTEVIAIIRKQNTYCYRRAVAVOKAANGHYRKAFKSHVSTLTDLOXYMOQFAHL	780
QY	781	QETSPRLDAVYIEOSSSLNEASSGFLFVFLRPMCNAHVRIRIGKSYVQCGIPQGISLTL	840
Db	781	QETSPRLDAVYIEOSSSLNEASSGFLFVFLRPMCNAHVRIRIGKSYVQCGIPQGISLTL	840
QY	841	LCSLCYGMEMKULRAGIRRDGILLRLVDDFLILNPHLTHACTFLTYVRGYPVEGCVNL	900
Db	841	LCSLCYGMEMKULRAGIRRDGILLRLVDDFLILNPHLTHACTFLTYVRGYPVEGCVNL	900
QY	901	RKTIVNPFVEDEALGSLAFVQMPAHGLPWCGLLIDTTLTEVQSDYSYSYASTISRATF	960
Db	901	RKTIVNPFVEDEALGSLAFVQMPAHGLPWCGLLIDTTLTEVQSDYSYSYASTISRATF	960
QY	961	NRGFRAGNNRRKULFVULRLKCHSLFDLDVNSLQVCTNYKILLLQAFYFHAQVLOLF	1020
Db	961	NRGFRAGNNRRKULFVULRLKCHSLFDLDVNSLQVCTNYKILLLQAFYFHAQVLOLF	1020
QY	1021	FHQQVWKQPTFFLRVYSDTASLCYSILKAKYAGMSLGAKGAAGPLPSEAVOMLGHQAFLL	1080
Db	1021	FHQQVWKQPTFFLRVYSDTASLCYSILKAKYAGMSLGAKGAAGPLPSEAVOMLGHQAFLL	1080
QY	1081	KLTRRRVTVVPLGSLRTAQOTLSKRLPGTTLTALAAANPALBDFEFTIID	1132
Db	1081	KLTRRRVTVVPLGSLRTAQOTLSKRLPGTTLTALAAANPALBDFEFTIID	1132

AC	ADG90599;
XX	
DT	25-MAR-2004 (first entry)
DE	Human TERT SEQ ID NO:2.
XX	
KW	human; immune response; telomerase reverse transcriptase; TERT;
KX	cyclostatic; immunostimulant; cancer; cytotoxic T cell response.
XX	
OS	Homo sapiens.
EN	WO2004002406-A2.
PD	
PF	24-JUN-2003; 2003WO-US019844.
XX	
PR	27-JUN-2002; 2002US-0393295P.
XX	
PA	(GERO-) GERON CORP.
PI	Majumdar A, Feather IA, Frolkis M, Wang Z,
DR	WI: 2004-071946/07.
NFSD:	ADG90598.
PT	Eliciting an immune response in a mammal specific for its own telomerase
FT	reverse transcriptase (TERT), useful for treating or preventing cancer,
FT	comprises administering a composition containing TERT of another
XX	mammalian species.
BS	Claim 66; SEQ ID NO 2; 4pp; English.
XX	
CC	The invention relates to a novel method for eliciting an immune response
CC	in a mammalian subject that is specific for its own telomerase reverse
CC	transcriptase (TERT), comprising administering an immunogenic composition
CC	containing a protein with at least 20 consecutive amino acids of TERT of
CC	another mammalian species, or a nucleic acid encoding the protein. A
CC	composition of the invention has cyclostatic, and immunostimulant
CC	activity. The protein or the nucleic acid encoding the protein is useful
CC	in the manufacture of a medicament for the treatment of cancer in a human
CC	or for eliciting a cytotoxic T cell response in a human.
XX	
SQ	Sequence 1132 AA:
Query Match	99.8%; Score 5952; DB 8; Length 1132;
Best Local Similarity	99.8%; Pred. No. 0;
Matches 1130; Conservative	1; Mismatches 1; Indels 0; Gaps 0;
QY	1 MPRAAPRCRAVSLRLSHYREVLPATFVRRLPGOGMRLVQRGDPPAFAFYAOCLVCVPM 60
DB	1 MPRAAPRCRAVSLRLSHYREVLPATFVRRLPGOGMRLVQRGDPPAFAFYAOCLVCVPM 60
QY	61 DARPPAAPSRROYSCKEIVARVLQRLCEBGAKNVALFGFALIDGARGPPEATTSVR 120
DB	61 DARPPAAPSRROYSCKEIVARVLQRLCEBGAKNVALFGFALIDGARGPPEATTSVR 120
QY	121 SYLPTVTDALRGSGAMGLLRVGDDVLVHLARCALFVLVAPSCAVOYCGPPLYOLGA 180
DB	121 SYLPTVTDALRGSGAMGLLRVGDDVLVHLARCALFVLVAPSCAVOYCGPPLYOLGA 180
QY	181 ATQAAPPFHAGPRRRLCCERANMHSVEAGVPICLPAGARRGGASRSRSLPKRRR 240
DB	181 ATQAAPPFHAGPRRRLCCERANMHSVEAGVPICLPAGARRGGASRSRSLPKRRR 240
QY	241 GAAPPERTPVGGGSWAHPGRTRGSDRGFCVSPARPABEATSLEGALSGTRHSPSVG 300
DB	241 GAAPPERTPVGGGSWAHPGRTRGSDRGFCVSPARPABEATSLEGALSGTRHSPSVG 300
QY	301 RQHNAAGPSTRRPRPMDTPCPVYAETKHFLLYSGGDEQLRPSTFLSSLPSTLGARRL 360
DB	301 RQHNAAGPSTRRPRPMDTPCPVYAETKHFLLYSGGDEQLRPSTFLSSLPSTLGARRL 360

QY 361 VETIFGSRPMWPGTBRRLRLRLRYWQWREPLLELGNHACQYGVLLKTHCPRAAVT 420
 Db 361 VETIFGSRPMWPGTBRRLRLRLRYWQWREPLLELGNHACQYGVLLKTHCPRAAVT 420
 QY 421 PAAGVCAKREKPGSVAAPEEEDTDRRLVQLRQSSPMQYGFVACLRRLVPPGLMGS 480
 Db 421 PAAGVCAKREKPGSVAAPEEEDTDRRLVQLRQSSPMQYGFVACLRRLVPPGLMGS 480
 QY 481 RINERERFLANTKKFISLGHAKLSIQELTWKSVDCAMLRSPGVCPAAEHLREBI 540
 Db 481 RINERERFLANTKKFISLGHAKLSIQELTWKSVDCAMLRSPGVCPAAEHLREBI 540
 QY 541 LAKFLHMLMSYVVELLRSEFFVETTTFOKRLFFYRPSVSKLSIGIRHLKRVQURE 600
 Db 541 LAKFLHMLMSYVVELLRSEFFVETTTFOKRLFFYRPSVSKLSIGIRHLKRVQURE 600
 QY 601 LSEAEVROREARPAALLTSRLRFIPKPDGLPIVNDYVGAARTRRKARLTSRYKA 660
 Db 601 LSEAEVROREARPAALLTSRLRFIPKPDGLPIVNDYVGAARTRRKARLTSRYKA 660
 QY 661 LFSVLYNEARBPGLLGASVGLDIDIRAMRTFVLRAADPPPELVFKVDVTCAYDTI 720
 Db 661 LFSVLYNEARBPGLLGASVGLDIDIRAMRTFVLRAADPPPELVFKVDVTCAYDTI 720
 QY 721 PODRLTEVIASIKQNTYCVRRYAVVQKAAHGRKAKFKSHVSTLTDLQSYMEQVANH 780
 Db 721 PODRLTEVIASIKQNTYCVRRYAVVQKAAHGRKAKFKSHVSTLTDLQSYMEQVANH 780
 QY 781 OETSPRLDVAVEOSSSINEASSGUPVETLRMCNHAARIGKSVQOCQIPQGSIIITL 840
 Db 781 OETSPRLDVAVEOSSSINEASSGUPVETLRMCNHAARIGKSVQOCQIPQGSIIITL 840
 QY 841 LQSLCGDMENKLPAGIRRDGLLRLVDLVLVTHLTHAKFTLTLVGVPEXCVNL 900
 Db 841 LQSLCGDMENKLPAGIRRDGLLRLVDLVLVTHLTHAKFTLTLVGVPEXCVNL 900
 QY 901 RKTVNFPEEDALGTAFAVQMPAGLPPWGLLIDTLEVOQSYSSYATSTRASITF 960
 Db 901 RKTVNFPEEDALGTAFAVQMPAGLPPWGLLIDTLEVOQSYSSYATSTRASITF 960
 QY 961 NNGFAGRMRRKRLFGVLRKCHSLFLDQVNSLQTVGCNIIYKILLQAYEFHACVQLP 1020
 Db 961 NNGFAGRMRRKRLFGVLRKCHSLFLDQVNSLQTVGCNIIYKILLQAYEFHACVQLP 1020
 QY 1021 FHQQVWKNFTFPLRVIYSDTASLCYILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080
 Db 1021 FHQQVWKNFTFPLRVIYSDTASLCYILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080
 QY 1081 KLTRHRVTVPPLGSLRTAQOTLSRKLPGTTLTALAAANPALPSPDFTIID 1132
 Db 1081 KLTRHRVTVPPLGSLRTAQOTLSRKLPGTTLTALAAANPALPSPDFTIID 1132
 RESULT 22
 AD182172
 ID AD182172 standard; protein; 1132 AA.
 AC AD182172;
 XX
 XX 22-APR-2004 (first entry)
 DT
 DE Human telomerase reverse transcriptase.
 XX
 XX Human, embryonic stem cell; pluripotent stem cell; abnormal cell growth;
 KW malignancy; differentiation.
 OS Homo sapiens.
 XX
 XX US2003224411-A1.
 PN
 XX 04-DEC-2003.
 PD
 XX 13-MAR-2003; 2003US-00388578.
 PF

XX 13-MAR-2003; 2003US-00388578.
 PR
 XX (STANTON L W.
 PA (BRAN) BRANDENBERGER R.
 PA (GOLD) GOLD J D.
 PA (IRVI) IRVING J M.
 PA (MAND) MANDALAM R.
 PA (MOKM) MOK M.
 PA (SHEL) SHELTON D.
 XX
 PI Stanton LM, Brandenberger R, Gold JD, Irving JM, Mandalam R;
 PI Mok M, Shelton D;
 XX
 DR WPI: 2004-119701/12.
 DR N-PSDB; AD182171.
 XX
 XX Assessing culture of undifferentiated primate pluripotent stem cells by
 PT detecting expression of markers e.g., Zic family member 3, other than
 PT human telomerase reverse transcriptase/octamer binding transcription
 PT factor.
 XX
 PS Claim 1; SEQ ID NO 2; 106bp; English.
 XX
 CC The invention relates to assessing a culture of undifferentiated primate
 CC pluripotent stem cells (PES, e.g. embryonic stem cells), involving
 CC detecting expression of markers (MR1) e.g. Zic family member 3 (ZIC3), as
 CC given in specification, other than human telomerase reverse transcriptase
 CC (hTERT) or octamer binding transcription factor (Oct) 3/4, or a marker
 CC (MR2) such as, cripto or podocalyxin-like protein and hTERT and/or Oct3/4
 CC or second marker chosen from (MR2). Also included are maintaining (M2)
 CC PES cells in a pluripotent state (involves causing them to express one of
 CC the following markers (MR3) at a higher level, FOXO1A, ZIC3, hypothetical
 CC protein FLJ20582, Forkhead box H1 (FOXH1), Zinc finger protein, Hsa12,
 CC KXAB-zinc finger protein SZF1-1 or zinc finger protein of cerebellum
 CC ZIC2, or any other marker (MR4) chosen from PHD protein Ude-1 (Ude-1),
 CC Kruppel-like zinc finger protein (ZNF300), etc., as given in the
 CC specification), causing PES cells to differentiate into a particular
 CC tissue type by causing them to express one of the markers chosen from
 CC (MR3) or (MR4) (or markers chosen from GATA binding protein 3 (GATA3),
 CC core promoter element binding protein (CPEB3), etc., as given in the
 CC specification), maintaining PES cells in a pluripotent state (involves
 CC culturing PES cells or their progeny in the presence of a normally
 CC secreted protein that is encoded by a gene that down-regulated upon
 CC differentiation of human embryonic stem (hES) cells, chosen from
 CC Fibrillin 3 gene, LEFT B gene, ZIC3 gene, EphA1 gene, etc., as given in
 CC the specification), causing PES cells to differentiate (involves
 CC culturing PES cells or their progeny in the presence of a normally
 CC secreted protein that is encoded by a gene that up-regulated upon
 CC differentiation of hES cells, chosen from p31 protein gene, Tax
 CC interaction protein 1 gene, KIA0893 protein gene, keratin 19 (KRT 19)
 CC gene, etc., as given in the specification), causing an encoding sequence
 CC to be preferentially expressed in undifferentiated PES cells, causing an
 CC encoding sequence to be preferentially expressed in differentiated cells,
 CC sorting (M4) differentiated cells from less differentiated cells
 CC (involves separating cells expressing a surface marker chosen from any
 CC one of MR1 from cells not expressing the marker), causing PES cells to
 CC proliferate without differentiation, identifying genes that are up or
 CC down regulated during differentiation of PES cells, and a kit (I) for
 CC assessing a culture of PES cells by M1. The method (M1) is useful for
 CC assessing culture of undifferentiated primate pluripotent stem cells and
 CC for assessing the growth characteristics of a cell population. The cell
 CC population has been obtained by culturing cells from human blastocyst or
 CC from a human patient suspected of having a clinical condition related to
 CC abnormal cell growth. The method further involves determining whether the
 CC cell population is pluripotent from the marker expression and assessing
 CC whether the patient has a malignancy from the marker expression. The
 CC present sequence is a protein whose expression is down regulated in
 CC pluripotent stem cells.
 XX
 SO Sequence 1132 AA;

Query Match

99.8%; Score 5952; DB 8; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MPRAACRAVSLRSHYREVLPATFVRRLGPGQGRVLVGRGPAAPRALVAOCLVCPW 60
DB 1 MPRAACRAVSLRSHYREVLPATFVRRLGPGQGRVLVGRGPAAPRALVAOCLVCPW 60
QY 61 DARPAPAPSFQVSCIKELVAVLQRLCERGAKNVLAFAFALLDGAAGGPPAFTTSVR 120
DB 61 DARPAPAPSFQVSCIKELVAVLQRLCERGAKNVLAFAFALLDGAAGGPPAFTTSVR 120
QY 121 SYLPTVYTDALRSGGAWGLLRVGGDVVHLIARCALFVLVAPSCAYQCGEPYQLQA 180
DB 121 SYLPTVYTDALRSGGAWGLLRVGGDVVHLIARCALFVLVAPSCAYQCGEPYQLQA 180
QY 181 ATQARPPHAGRRRLGCEKAMNHSYREAGVPLGAPAGARRGGASASLPLRKRPRR 240
DB 181 ATQARPPHAGRRRLGCEKAMNHSYREAGVPLGAPAGARRGGASASLPLRKRPRR 240
QY 241 GAAPBEPRTPVGGGSMWHPGRTGSPDRGFCVYSPAPAEATSLGALSGTRHSPSVG 300
DB 241 GAAPBEPRTPVGGGSMWHPGRTGSPDRGFCVYSPAPAEATSLGALSGTRHSPSVG 300
QY 301 ROHHAGPSTSRPPRMDTQCPVYAEKHLVSGDKQLRSPFLSSLRPSLTGARL 360
DB 301 ROHHAGPSTSRPPRMDTQCPVYAEKHLVSGDKQLRSPFLSSLRPSLTGARL 360
QY 361 VETIFLGSRPMDGTPLRLPQRYWOKRPLFLELIGNHACQCPYGLLKTGCPLEAAVT 420
DB 361 VETIFLGSRPMDGTPLRLPQRYWOKRPLFLELIGNHACQCPYGLLKTGCPLEAAVT 420
QY 421 PAAGVCAKREKQSSVAAPBEEDTPRLVOLLRQSSPMQVYGFVACLRVLPGLMGS 480
DB 421 PAAGVCAKREKQSSVAAPBEEDTPRLVOLLRQSSPMQVYGFVACLRVLPGLMGS 480
QY 481 RHNERPFLRNTKFFISLGHAKLSLOELTWKMSVRCAMLRSPGVCPAAEHRRLREBI 540
DB 481 RHNERPFLRNTKFFISLGHAKLSLOELTWKMSVRCAMLRSPGVCPAAEHRRLREBI 540
QY 541 LAFELHMSVYVELLSFFVYETTFQKNRLFFRPSVSKLQSIGIRQLKRYQLE 600
DB 541 LAFELHMSVYVELLSFFVYETTFQKNRLFFRPSVSKLQSIGIRQLKRYQLE 600
QY 601 LSAEVRQHEARPAALTSRLRFPKDPGRPIVNMVYVGAATFRERARELTSRYVA 660
DB 601 LSAEVRQHEARPAALTSRLRFPKDPGRPIVNMVYVGAATFRERARELTSRYVA 660
QY 661 LFSVLNVERARBPGLLGASVGLDDIHRAMRTFVLNRACQDPPELIFYKVDVTGAYDI 720
DB 661 LFSVLNVERARBPGLLGASVGLDDIHRAMRTFVLNRACQDPPELIFYKVDVTGAYDI 720
QY 721 PQRRLLEVASLITKQNTYCVRRYAVVQRAAHGHVAKAFKSHVSTLTDIOPWRQVAML 780
DB 721 PQRRLLEVASLITKQNTYCVRRYAVVQRAAHGHVAKAFKSHVSTLTDIOPWRQVAML 780
QY 781 QETSPRLDAVIRQSSSLNEASGLFDVFLRFMCHNAVRIRGSGYQCGIPQGSILSTL 840
DB 781 QETSPRLDAVIRQSSSLNEASGLFDVFLRFMCHNAVRIRGSGYQCGIPQGSILSTL 840
QY 841 LQSLCAGDMENKLPAGIRRDGLLRLVDDFLVTLTAKFTLRLTVAGVEYGCVMVL 900
DB 841 LQSLCAGDMENKLPAGIRRDGLLRLVDDFLVTLTAKFTLRLTVAGVEYGCVMVL 900
QY 901 RKTVAAPFVDEDLGGTAFAVQMPAHGLFPWCGLLTRTLEVSQDVSSVARSIRASVTF 960
DB 901 RKTVAAPFVDEDLGGTAFAVQMPAHGLFPWCGLLTRTLEVSQDVSSVARSIRASVTF 960
QY 961 NRGFKAQRNRKRLFGVLRILKCHSLFLDQVNSLQTCVCTNIYKILLQAYRFAVCLQLP 1020
DB 961 NRGFKAQRNRKRLFGVLRILKCHSLFLDQVNSLQTCVCTNIYKILLQAYRFAVCLQLP 1020
QY 1021 FHOQWKNPFELRVISDTSILCYSTILKAKNAGMSLGAKGAGPLSEAVOMLCHQAFLL 1080
DB 1021 FHOQWKNPFELRVISDTSILCYSTILKAKNAGMSLGAKGAGPLSEAVOMLCHQAFLL 1080

```

```

DB 1021 FHOQWKNPFELRVISDTSILCYSTILKAKNAGMSLGAKGAGPLSEAVOMLCHQAFLL 1080
QY 1081 KLTRHRYVYVPLIGSLRTAQOTLSRKLPGLTTLTLEAANALSDPFTIID 1132
DB 1081 KLTRHRYVYVPLIGSLRTAQOTLSRKLPGLTTLTLEAANALSDPFTIID 1132
RESULT 23
AAW61350
ID AAW61350 standard; protein, 1154 AA.
XX
AC AAW61350;
XX
DT 25-MAR-2003 (revised)
DT 12-OCT-1998 (first entry)
XX
DE Human telomerase protein 2 (TP2).
XX
KM TP2, human; telomerase protein 2; cancer; AIDS; ageing; therapy.
XX
OS Homo sapiens.
XX
PN WO9821343-A1.
PD 22-MAY-1998.
XX
PF 13-NOV-1997; 97WO-US021248.
XX
PR 15-NOV-1996; 96US-00751189.
PR 11-JUN-1997; 97US-008473039.
PR 16-OCT-1997; 97US-00951733.
XX
PA (AMGE-) AMGEN INC.
PA (AMGE-) AMGEN CANADA INC.
XX
PI Harrington LA, Robinson MO;
PI WPI: 1998-297946/26.
DR N-PSDB; AAV27876.
XX
PT New nucleic acid encoding human telomerase protein-2 - used for
PT regulating telomerase activity, e.g. for treating cancer or acquired
PS immune deficiency syndrome.
XX
PS Claim 1e; Fig 9; 150pp; English.
XX
CC This polypeptide comprises human telomerase protein 2 (TP2), a novel
CC protein of the telomerase complex. Its amino acid sequence was deduced
CC from a composite (see AAV27876) of isolated cDNA clones 32 (see AAV27872)
CC and TP2-15 (see AAV27875), obtained from a human colon tumour cell line
CC LIM863 cDNA. Expressing TP2 in a cell is used to increase telomerase
CC activity and thus proliferation for treatment of e.g. HIV infection, AIDS
CC and ageing disorders, while expressing an inactive mutant of TP2 (or
CC molecule antisense to the gene) is used to decrease telomerase activity,
CC e.g. for treatment of cancer. TP2 polypeptides can also be used to screen
CC for agents that inhibit TP2 activity or its binding to TRIP1 (see
CC AAW61347) or telomerase RNA, potentially useful therapeutically, also to
CC raise specific antibodies useful in immunoassays and therapeutically as
CC inhibitors. Also contemplated are transgenic animals in which the TP2
CC gene has been inactivated or is overexpressed. TP2 polypeptides are
CC administered i.v., s.c. or orally, or they are delivered from engineered
CC cells or gene therapy vectors. (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 1154 AA.

```

Query Match 99.8%; Score 5952; DB 2; Length 1154;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MPRAACRAVSLRSHYREVLPATFVRRLGPGQGRVLVGRGPAAPRALVAOCLVCPW 60
DB 23 MPRAACRAVSLRSHYREVLPATFVRRLGPGQGRVLVGRGPAAPRALVAOCLVCPW 82

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QY 61 DARPAPAPSPROVCLKEIVARVLQRLCERGAKNVLAFGFALLDGAAGGPEAFTTSVR 120
DB 83 DARPAPAPSPROVCLKEIVARVLQRLCERGAKNVLAFGFALLDGAAGGPEAFTTSVR 142
QY 121 SYLENTVTDALGSGAMGILLRRVGDVLAHLLARCALFVVAAPCAVQVGPPELYOUGA 180
DB 143 SYLENTVTDALGSGAMGILLRRVGDVLAHLLARCALFVVAAPCAVQVGPPELYOUGA 202
QY 181 ATQAPPPHASPGRRLGGERAMNSVBAVPLGLPAPGARRRRGSASRLPJKPERR 240
DB 203 ATQAPPPHASPGRRLGGERAMNSVBAVPLGLPAPGARRRRGSASRLPJKPERR 262
QY 241 GAAPBERTPVQGGSWAHPDRTGPSDRGFCVSPAPAEBAATSLGALSGTRISHSPVG 300
DB 263 GAAPBERTPVQGGSWAHPDRTGPSDRGFCVSPAPAEBAATSLGALSGTRISHSPVG 322
QY 301 RQHHAGPSTSPRPWPDPCCPVAAETGKFLYSSGDXEOLRPSFILSLRPSLTGARL 360
DB 323 RQHHAGPSTSPRPWPDPCCPVAAETGKFLYSSGDXEOLRPSFILSLRPSLTGARL 382
QY 361 VETIFLGSRPMMPGTERRLPRLPQRYWQWRPLFELLGNHAOCYPYVLLKTHCPIDRAVT 420
DB 383 VETIFLGSRPMMPGTERRLPRLPQRYWQWRPLFELLGNHAOCYPYVLLKTHCPIDRAVT 442
QY 421 PAAGVABRKPQGSVAAPREEDTDPRVLQRLRQSSPMOYGFYRACLRRLVPPGLMGS 480
DB 443 PAAGVABRKPQGSVAAPREEDTDPRVLQRLRQSSPMOYGFYRACLRRLVPPGLMGS 502
QY 481 RHNERFLNTRKFFISLGKAKLSLOELTKMSVBCAMLRSPGCVPAAEHRLREI 540
DB 503 RHNERFLNTRKFFISLGKAKLSLOELTKMSVBCAMLRSPGCVPAAEHRLREI 562
QY 541 LAKFLHMLSVYVVELLRFFVYTTTQKRLFFYRPSWSKLOSIGIOLHKLKRVQURE 600
DB 563 LAKFLHMLSVYVVELLRFFVYTTTQKRLFFYRPSWSKLOSIGIOLHKLKRVQURE 622
QY 601 LSAEAVROREARPALLTRSLRFPKPDGLRPIVMMDYVVGARTREKAERLTSRYKA 660
DB 623 LSAEAVROREARPALLTRSLRFPKPDGLRPIVMMDYVVGARTREKAERLTSRYKA 682
QY 661 LFSVLYNERARPPGLIGASVLGLDDIHRAMRTFVLRAODPPPLVYVVDVGTAVYTI 720
DB 683 LFSVLYNERARPPGLIGASVLGLDDIHRAMRTFVLRAODPPPLVYVVDVGTAVYTI 742
QY 721 PODRLTEVIASTIKPONTVCARVAVVOGAHGRKAKFKSHVSTLTLOPYMRQFVAHL 780
DB 743 PODRLTEVIASTIKPONTVCARVAVVOGAHGRKAKFKSHVSTLTLOPYMRQFVAHL 802
QY 781 QETSPLRDAVIEOSSSLNEASSGLFDFVFLRMCHHAAVIRKGSYVQCQGIPOGSIISTL 840
DB 803 QETSPLRDAVIEOSSSLNEASSGLFDFVFLRMCHHAAVIRKGSYVQCQGIPOGSIISTL 862
QY 841 LGSICGDEVENTLFAIRRDGILLRLVDFELVTBHLTHAKTEFLTRVGVPEVGCYVNL 900
DB 863 LGSICGDEVENTLFAIRRDGILLRLVDFELVTBHLTHAKTEFLTRVGVPEVGCYVNL 922
QY 901 RKTVPVFPEDBALGGTAFCVQWPAHGLFPWCGLIDTRLTEVOSDYSSYARTSIRASYTF 960
DB 923 RKTVPVFPEDBALGGTAFCVQWPAHGLFPWCGLIDTRLTEVOSDYSSYARTSIRASYTF 982
QY 961 NNGFKAGRMWRKRLFEVLRKCHSLFDLDQVNSLQTVCTNIIKILLQAYRHAVALDLP 1020
DB 983 NNGFKAGRMWRKRLFEVLRKCHSLFDLDQVNSLQTVCTNIIKILLQAYRHAVALDLP 1042
QY 1021 FHQOVKNPFLPFLRVSDTASLCYSILKAKNAGMSIGAKAGAPLPSSAVQLCHQATLL 1080
DB 1043 FHQOVKNPFLPFLRVSDTASLCYSILKAKNAGMSIGAKAGAPLPSSAVQLCHQATLL 1102
QY 1081 KLTRHRTVVPPLIGSLRTAQOTLSRKLPGTTLTALAAANPALPSDFXTIID 1132
DB 1103 KLTRHRTVVPPLIGSLRTAQOTLSRKLPGTTLTALAAANPALPSDFXTIID 1154

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```

RESULT 24
AAM47008
ID AAM47008 standard; protein; 1189 AA.
XX
AC AAM47008:
XX
DT 13-AUG-1998 (first entry)
XX
DE Glutathione-S-transferase and hTERT fusion protein 8.
XX
KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 22..23
FT /note="enterokinase cleavage site"
XX
PN GB2317891-A.
XX
PD 08-APR-1998.
XX
PE 01-OCT-1997; 97GB-00020890.
XX
PR 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Langer J, Nakamura T, Chapman KB, Morin GB, Harley CB;
Andrews WH;
XX
DR WPI; 1998-171633/16.
XX
PT Pure and recombinant human telomerase Reverse Transcriptase and its
variants - are useful in the diagnosis, prognosis and treatment of cell
proliferation conditions especially cancer and ageing.
XX
PS Example 6; Page 234-235; 387pp; English.
XX
CC The present sequence represents a fusion protein from an example of the
present invention which describes human telomerase reverse transcriptase
(hTERT). The present invention also describes the following methods: (A)
determining whether a test compound is a modulator of hTERT, by detecting
the change in hTERT recombinant protein or polynucleotide, on
administration of the compound; (B) preparation of recombinant telomerase
by contacting a protein preparation of hTERT with a telomerase RNA
component; (C) detection of the hTERT RNA or protein in a sample by
binding a relevant probe to the sample and detecting the complex formed
or in the case of RNA detection, amplifying the product and correlating
the presence of complex or amplification product with presence of hTERT in
the sample; and (D) increasing the proliferation of a vertebrate cell by
increasing hTERT expression; and (E) the use of an agent that causes an
increase in cell vertebrate cell proliferation to create a medicament
that inhibits ageing. A protein preparation of hTERT and the
polynucleotide encoding hTERT can be used in the manufacture of
medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
telomerase activity can be used to treat conditions that are associated
with high telomerase activity. A protein preparation of hTERT can also be
used in the new methods
CC Sequence 1189 AA;
XX
SQ

```

Query Match 99.8%; Score 5952; DB 2; Length 1189;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLSRSHREVLPLATFVRRLSGQGRVORGGPAPAFALVQCIVCW 60
 DB 58 MPAPRCRAVRSLSRSHREVLPLATFVRRLSGQGRVORGGPAPAFALVQCIVCW 117

QY 61 DAEPAPAPSPFQVSCIKELVAZVLCRCGAKNYLAFGALLDARGGPEAPFTSVR 120
 DB 118 DAEPAPAPSPFQVSCIKELVAZVLCRCGAKNYLAFGALLDARGGPEAPFTSVR 177

QY 121 SYLPNTVTDLRSGGAMGLLRVGDVVLHLLARCALPLVAPSCAYQVCGPPLYLGA 180
 DB 178 SYLPNTVTDLRSGGAMGLLRVGDVVLHLLARCALPLVAPSCAYQVCGPPLYLGA 237

QY 181 ATQARPBPASGPRRLGCEBAMNHSVREAGVPLGAPGARRRGSSASRSLPLRPRPR 240
 DB 238 ATQARPBPASGPRRLGCEBAMNHSVREAGVPLGAPGARRRGSSASRSLPLRPRPR 297

QY 241 GAAPPEBRTFVGGGSAHPGRTGSPSDRGFCVSPAPABEATSLGALSGTRHSPSVG 300
 DB 298 GAAPPEBRTFVGGGSAHPGRTGSPSDRGFCVSPAPABEATSLGALSGTRHSPSVG 357

QY 301 RQHHAGPSTSRPPRMDTFCPPVYAEKHFYLSGDKQLRSPFLLSLRPSLTGARL 360
 DB 358 RQHHAGPSTSRPPRMDTFCPPVYAEKHFYLSGDKQLRSPFLLSLRPSLTGARL 417

QY 361 VETIFLGSRPMDGTPLRLPLPQRYQWMLFLELLGNHAGCPYVLLKTHCPLRAAVT 420
 DB 418 VETIFLGSRPMDGTPLRLPLPQRYQWMLFLELLGNHAGCPYVLLKTHCPLRAAVT 477

QY 421 PAAGVAREKPGSVAPAEEDDPRLVOLLRQSSPMQVYGFVACRLRPLPGLMGS 480
 DB 478 PAAGVAREKPGSVAPAEEDDPRLVOLLRQSSPMQVYGFVACRLRPLPGLMGS 537

QY 481 RHNERFLRNTKFFISLGKAKLSLOELTKMSVRCAMLRSPGVGCVPAAEHRLREI 540
 DB 538 RHNERFLRNTKFFISLGKAKLSLOELTKMSVRCAMLRSPGVGCVPAAEHRLREI 597

QY 541 LAFLHMLSVYVVELLSRFFYTETTPQKNRLFPPRPYSWGLQSIGRQHKRYQRE 600
 DB 598 LAFLHMLSVYVVELLSRFFYTETTPQKNRLFPPRPYSWGLQSIGRQHKRYQRE 657

QY 601 LSAEVRQREAPALTLSTRFLPKPDGRPIVMNDYVVGARTFERREKAEHLSTRVA 660
 DB 658 LSAEVRQREAPALTLSTRFLPKPDGRPIVMNDYVVGARTFERREKAEHLSTRVA 717

QY 661 LBSVLNYSRRRFGLLGASVGLDIDIRAMRTFVLVRADQPEPPELVFKVVDVTAADTI 720
 DB 718 LBSVLNYSRRRFGLLGASVGLDIDIRAMRTFVLVRADQPEPPELVFKVVDVTAADTI 777

QY 721 PQRLREVLASILKQNTQVRRYAVVOKAAAGHVAKAFKSHSTLTDIOPYRQCVATL 780
 DB 778 PQRLREVLASILKQNTQVRRYAVVOKAAAGHVAKAFKSHSTLTDIOPYRQCVATL 837

QY 781 QETSPLRDVAVIEQSSSLNEASSGLFVPLRFMCHNAVIRGKSYVQCQIGISLSTL 840
 DB 838 QETSPLRDVAVIEQSSSLNEASSGLFVPLRFMCHNAVIRGKSYVQCQIGISLSTL 897

QY 841 LGSLLCGDMENKLPAGIRRDGGLLRVDLFLVTHPLTHAKTFLRLVNGVEYGVVNL 900
 DB 898 LGSLLCGDMENKLPAGIRRDGGLLRVDLFLVTHPLTHAKTFLRLVNGVEYGVVNL 957

QY 901 RKTVMFPVEDEALGTAFAVQMPAHGLFPWCGLLLTRTLTEVQSDVSSAFARSIRASVFP 960
 DB 958 RKTVMFPVEDEALGTAFAVQMPAHGLFPWCGLLLTRTLTEVQSDVSSAFARSIRASVFP 1017

QY 961 NRGPFKAGRMNRRLFGVLRKCHSLFLDIQVNSLQVTCNIIYKILLQAYRHACYQLP 1020
 DB 1018 NRGPFKAGRMNRRLFGVLRKCHSLFLDIQVNSLQVTCNIIYKILLQAYRHACYQLP 1077

QY 1021 FHOQWKNPTFFLRVISTDASLGYSLIKKANAGMSLGAGGAQPLBSEAVQWLCHQAFLL 1080

DB 1078 FHOQWKNPTFFLRVISTDASLGYSLIKKANAGMSLGAGGAQPLBSEAVQWLCHQAFLL 1137
 QY 1081 KLTRRATVYVPLLSGLRPAQTQLSRKLPGTTLTLEAANALPSPDFKTIID 1132
 DB 1138 KLTRRATVYVPLLSGLRPAQTQLSRKLPGTTLTLEAANALPSPDFKTIID 1169

RESULT 25
 AA47000
 ID AA47000 standard; protein; 1285 AA.

AA47000;
 13-AUG-1998 (first entry)

HIS tagged thioredoxin moiety and full length hTERT fusion protein.
 Human, telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 cell proliferation; cancer; ageing; ribonucleoprotein.

Synthetic.
 Homo sapiens.

Key location/Qualifiers
 Misc-difference 119..120
 /note="nucleokinase cleavage site"
 120..1285
 Region /label="hTERT
 /note="full length human telomerase reverse
 transcriptase"

GB2317891-A.
 08-APR-1998.
 01-OCT-1997; 97GB-00020890.
 01-OCT-1996; 96US-00724643.
 18-APR-1997; 97US-00844419.
 25-APR-1997; 97US-00846017.
 06-MAY-1997; 97US-00851843.
 09-MAY-1997; 97US-00854050.
 14-AUG-1997; 97US-00911312.
 14-AUG-1997; 97US-00912951.
 14-AUG-1997; 97US-00915503.

(GERO-) GERON CORP.
 (UYTE-) UNIV TECHNOLOGY CORP.
 Cecch TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB,
 Andrews WH;
 WPL, 1998-171633/16.

Pure and recombinant human Telomerase Reverse Transcriptase and its
 variants - are useful in the diagnosis, prognosis and treatment of cell
 proliferation conditions especially cancer and ageing.

Example 6; Page 223; 387pp; English.

The present sequence represents a fusion protein from an example of the
 present invention which describes human telomerase reverse transcriptase
 (hTERT). The present invention also describes the following methods: (A)
 determining whether a test compound is a modulator of hTERT, by detecting
 the change in hTERT recombinant protein or polynucleotide, on
 administration of the compound; (B) preparation of recombinant telomerase
 by contacting a protein preparation of hTERT with a telomerase RNA
 component; (C) detection of the hTERT RNA or protein in a sample by
 binding a relevant probe to the sample and detecting the complex formed
 or in the case of RNA detection, amplifying the product and correlating
 the presence of complex or amplification product with presence of hTERT in
 the sample; and (D) increasing the proliferation of a vertebrate cell by

increasing hprt expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hprt and the polynucleotide encoding hprt can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hprt can also be used in the new methods

Sequence 1285 AA,

Query Match	99.7%	Score 5946	DB 2	Length 1285
Best Local Similarity	99.7%	Pred. No. 0		
Matches 1129	Conservative	1	Mismatches 2	Indels 0
			Gaps	0

Db	154	MPAPRCBAVRSLRSHREYVJPLATFVRLOPQGMRLVYRGDPAAPRAVAQIVCPVM	213
Qy	61	DABPPAABSFVOYGLKELVAVRLOICEGAKXVLAFCGALLDAGRGGBPEAFPTTSVR	120
Db	214	DABPPAABSFVYOSLKEVAVRLOICEERAKXVLEFGALLDAGRGGBPEAFPTTSVR	273
Qy	121	SYVJNTVTDALROSAGMGLLRVRVDVVLVLLARCALFVLVAESCAVOYCGPELVQLG	180
Db	274	SYVJNTVTDALROSAGMGLLRVRVDVVLVLLARCALFVLVAESCAVOYCGPELVQLG	333
Qy	181	ATQAPRPPHAGSGRRPLGGERAMNHSVEAGVPLPGAGRRRGASASLPLPKRPR	240
Db	334	ATQAPRPPHAGSGRRPLGGERAMNHSVEAGVPLPGAGRRRGASASLPLPKRPR	393
Qy	241	GAAPBEERTVQGGWAHFGATRGSDRGFCVVSAPAPAEATSLLEGALGSTRHSHSV	300
Db	394	GAAPBEERTVQGGWAHFGATRGSDRGFCVVSAPAPAEATSLLEGALGSTRHSHSV	453
Qy	301	ROHAGBPSTSRPPRMDTCCPPVVAETGHFLYSSGDKEQRPBFLSLSPSLTGARRL	360
Db	454	ROHAGBPSTSRPPRMDTCCPPVVAETGHFLYSSGDKEQRPBFLSLSPSLTGARRL	513
Qy	361	VEITFLGSRWMBGTBRRLPRLPORWQMRPLFLELLGNHAQCFYVILLKTCPLRAAVT	420
Db	514	VEITFLGSRWMBGTBRRLPRLPORWQMRPLFLELLGNHAQCFYVILLKTCPLRAAVT	573
Qy	421	PAGVCAAREPQGSVAAREEDTDPRRLVOLLROHSSWQVOYGVRACLRLVPGMG	480
Db	574	PAGVCAAREPQGSVAAREEDTDPRRLVOLLROHSSWQVOYGVRACLRLVPGMG	633
Qy	481	RHNERFLRNTKXFLISLGHAKLSLOBLTWKMSVDCAMLRSPQGVCPAPAEHRLREI	540
Db	634	RHNERFLRNTKXFLISLGHAKLSLOBLTWKMSVDCAMLRSPQGVCPAPAEHRLREI	693
Qy	541	LAKFLHMLMSVYVELLSFFVYETETPQXRLFPYRASVSKLOSIGIOHLKRYOLRE	600
Db	694	LAKFLHMLMSVYVELLSFFVYETETPQXRLFPYRASVSKLOSIGIOHLKRYOLRE	753
Qy	601	LSEAYRQHRBAPALLTSLRLFTPEKPDGLRIYVMDEVGARTPRRKRARLTSVK	660
Db	754	LSEAYRQHRBAPALLTSLRLFTPEKPDGLRIYVMDEVGARTPRRKRARLTSVK	813
Qy	661	LFSVLYTERARBRGGLGASVGLDITHRAMRFLVLRVAOORPELTFVKVDVTGAVDTI	720
Db	814	LFSVLYTERARBRGGLGASVGLDITHRAMRFLVLRVAOORPELTFVKVDVTGAVDTI	873
Qy	721	PODLTEVIASIIKPNQTVCVRRYAVVQKAAGHVRAKFSHVSITLDLOPYMFOVAHL	780
Db	874	PODLTEVIASIIKPNQTVCVRRYAVVQKAAGHVRAKFSHVSITLDLOPYMFOVAHL	933
Qy	781	QENSPRLDAVVIQSSSLNEASGFDVFLRMCHAVRIGKSVQOCQGIPOSSILSTL	840
Db	934	QENSPRLDAVVIQSSSLNEASGFDVFLRMCHAVRIGKSVQOCQGIPOSSILSTL	993
Qy	841	LSGLCGIDMENKFLPAGIRPDGLLRLVDFLLVTHLTHAKTPLRTVRYGVPIYGCYVNL	900

Db	994	LCSLCYGDMENKLFAGIRBDGILLRLVDDFLVLTPLHTHAKTFRLTVRGVEYXGVNLT	1053
Qy	901	RKYVNPVEVDEALGGAFTAVQMPRHGTFPMCGILLDRTLVEQSDGSAVATSRASVTF	960
Db	1054	RKYVNPVEVDEAAGGTAFTVQMPRHGTFPMCGILLDRTLVEQSDGSAVATSRASVTF	1113
Qy	961	NRGFKARNRRKRLFGVLRKCHSLFDLQVNSLQVCTNIYKILLQAVRFHACVQLQLP	1020
Db	1114	NRGFKARNRRKRLFGVLRKCHSLFDLQVNSLQVCTNIYKILLQAVRFHACVQLQLP	1173
Qy	1021	PHQVWKNPFFFLFVIGDITASLCSILKAKAGCSLAKGAAGLBPBAVQMLCHQAFLL	1080
Db	1174	PHQVWKNPFFFLFVIGDITASLCSILKAKAGCSLAKGAAGLBPBAVQMLCHQAFLL	1233
Qy	1081	KLTHRRVTVYVPLGSLRTAQFOLSRKLPGLTLLLEAANPALSPDEKTIYLD	1132
Db	1234	KLTHRRVTVYVPLGSLRTAQFOLSRKLPGLTLLLEAANPALSPDEKTIYLD	1285

```

RESULT 26
AAW71376
ID AAW71376 standard; protein: 1132 AA.
XX
AC AAW71376;
XX
DT 04-DEC-1998 (first entry)
XX
DE Human telomerase catalytic subunit referred to as hEST2.
XX
KW Catalytic subunit; human; telomerase; telomere maintenance; diagnosis;
RW treatment; cancer.
XX
OS Homo sapiens.
XX
PN M09837181-A2.
XX
PD 27-AUG-1998.
XX
PF 20-FEB-1998; 98WO-US003404.
XX
PR 20-FEB-1997; 97US-0038750P.
PR 20-MAY-1997; 97US-0047151P.
PR 01-AUG-1997; 97US-0054549P.
PR 14-AUG-1997; 97US-0055762P.
PR 30-OCT-1997; 97US-0064322P.
XX
PA (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Counter CM, Meyerson M, Weinberg RA;
XX
DR MPI: 1998-495367/42.
DR N-PSDB: AAV60320.
XX
FT New isolated human telomerase catalytic sub-unit gene - used to develop
FT products for increasing or reducing the life span of cells such as cancer
FT cells or transformed cells.
XX
PS Claim 5; Fig 6; 96pp; English.
XX
XX
XX The present sequence represents the catalytic subunit of a human
XX telomerase holoenzyme. Disruption of the telomerase gene alters telomere
XX maintenance. The DNA is essential for telomerase activity, and the
XX protein is physically associated with telomerase and a constituent of
XX active telomerase complex. The products can be used for increasing or
XX reducing the lifespan of cells such as cancer cells or transformed cells.
XX They can also be used in the diagnosis and treatment of malignancies. In
XX addition, cells with a longer lifespan can be transplanted into or
XX grafted onto an individual (e.g. as skin grafts, as systems for delivery
XX of therapeutic proteins, such as hormones and enzymes), to whom they
XX provide therapeutic benefit
XX
XX Sequence 1132 AA;
XX

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Db      1 MPRAPRCRAVRSILRSHYREVLPPLATFVRLRPGQGRVLVQSGDPAFRALVAQCLVCVPM 60
Qy      61 DARRPPAASFRVOSCLKEIVARVLORLCERGAKNVLAFGFLLDGAAGGPEAFTTSVR 120
Db      61 DARRPPAASFRVOSCLKEIVARVLORLCERGAKNVLAFGFLLDGAAGGPEAFTTSVR 120
Qy      121 SYLPNTVTDALRGSGAMGILLRRVGDVVLVHLAACAFLVLAAPSACAYQVCGPPLYOLGA 180
Db      121 SYLPNTVTDALRGSGAMGILLRRVGDVVLVHLAACAFLVLAAPSACAYQVCGPPLYOLGA 180
Qy      181 ATOQARPPHASPBRRLGGERAMNHSVRPAGVPLGPAAGARRRGASRSLLPKRRRR 240
Db      181 ATOQARPPHASPBRRLGGERAMNHSVRPAGVPLGPAAGARRRGASRSLLPKRRRR 240
Qy      241 GAAPBEPRTVQGSVAHAGRTGSDRGFCVSPAPPAEATSLGALSGTRHSHPEVG 300
Db      241 GAAPBEPRTVQGSVAHAGRTGSDRGFCVSPAPPAEATSLGALSGTRHSHPEVG 300
Qy      301 ROHHAQBPSTSRPPRWDTPCPPTVATKTHFLYSSGDKQLRPSGLSLRPSLTGARRL 360
Db      301 ROHHAQBPSTSRPPRWDTPCPPTVATKTHFLYSSGDKQLRPSGLSLRPSLTGARRL 360
Qy      361 VETIFLGSRPMMWGPTRRLPRLPORVQWRPLFLELGNHACQPGVLLKTHCPRLRAVLT 420
Db      361 VETIFLGSRPMMWGPTRRLPRLPORVQWRPLFLELGNHACQPGVLLKTHCPRLRAVLT 420
Qy      421 PAAGVACAREKPOGSVAAPBEECDTDRRLVOLLROHSSPMQYGFVRAQLRLVPPGLMGS 480
Db      421 PAAGVACAREKPOGSVAAPBEECDTDRRLVOLLROHSSPMQYGFVRAQLRLVPPGLMGS 480
Qy      481 RHNERRFLRNTKFFLSLGHAKLSLOELTWKMSVDCAMLRSPGVGVPAEHLRREI 540
Db      481 RHNERRFLRNTKFFLSLGHAKLSLOELTWKMSVDCAMLRSPGVGVPAEHLRREI 540
Qy      541 LAKETLHMLMSVYVVELLRSEFFVYETTFPOKNRLFEPYRPSVMSKLOSIGIRHOLKRVOLRE 600
Db      541 LAKETLHMLMSVYVVELLRSEFFVYETTFPOKNRLFEPYRPSVMSKLOSIGIRHOLKRVOLRE 600
Qy      601 LSEAEVRQREARPAALITSLRLEFIPKPGDLRIYVMDYVAGARTRREKAKARLTSRYKA 660
Db      601 LSEAEVRQREARPAALITSLRLEFIPKPGDLRIYVMDYVAGARTRREKAKARLTSRYKA 660
Qy      661 LFSVLYNERARPPGLLGAASVGLDDIHRAMRTFVLRVBAQDPPPLVYKVDVTAAYDTI 720
Db      661 LFSVLYNERARPPGLLGAASVGLDDIHRAMRTFVLRVBAQDPPPLVYKVDVTAAYDTI 720
Qy      721 PODRLTEVIASITIKPONTYCVARVAVOXAAGHVRKAFKSHVSTLTLOPYMRQFVAHL 780
Db      721 PODRLTEVIASITIKPONTYCVARVAVOXAAGHVRKAFKSHVSTLTLOPYMRQFVAHL 780
Qy      781 OETSPLRDVAVLEQSSSLNEASSGLFDVFLRFMCHAAVIRKGSIVYOCQGLPQGSILSTL 840
Db      781 OETSPLRDVAVLEQSSSLNEASSGLFDVFLRFMCHAAVIRKGSIVYOCQGLPQGSILSTL 840
Qy      841 LCSLCYGDMENTKLFAGIRRDGLLLRLVDDFLLVTEHLTHAKTFLRTIVRGVEYGCVVNL 900
Db      841 LCSLCYGDMENTKLFAGIRRDGLLLRLVDDFLLVTEHLTHAKTFLRTIVRGVEYGCVVNL 900
Qy      901 KRTVVNFPEDEALGATAVQMPAHGLPWCGLLDITRLEVOQSYSSVARTSIRASLTFF 960
Db      901 KRTVVNFPEDEALGATAVQMPAHGLPWCGLLDITRLEVOQSYSSVARTSIRASLTFF 960
Qy      961 NNGFYAGAMRRKRLFGVLRKCHSLFLDIQVNSLQTVCTNLYKIDLLQAYFHAQVLOLP 1020
Db      961 NNGFYAGAMRRKRLFGVLRKCHSLFLDIQVNSLQTVCTNLYKIDLLQAYFHAQVLOLP 1020
Qy      1021 FHQOQWKNPTFFLRVYISDTASLCYSILKAKAKAGSLGAKAAGPLPSAVALMLCHQAFLL 1080
Db      1021 FHQOQWKNPTFFLRVYISDTASLCYSILKAKAKAGSLGAKAAGPLPSAVALMLCHQAFLL 1080
Qy      1081 KLTRRRTVTVPLLGSILRTAQOTLSRKLPEPTLTALAEAAANPALPSPDFITIID 1132
Db      1081 KLTRRRTVTVPLLGSILRTAQOTLSRKLPEPTLTALAEAAANPALPSPDFITIID 1132

```

```

RESULT 28
AA00638
ID AA00638 standard; protein; 1132 AA.
XX
AC AA00638;
XX
DT 26-JUL-1999 (first entry)
XX
DE Truncated telomerase protein sequence.
XX
KM Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KM neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KM smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
KM stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WC0901560-A1.
XX
PD 14-JAN-1999.
XX
PF 01-JUL-1998; 98WO-US013835.
XX
PR 01-JUL-1997; 97US-0051410P.
PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0058287P.
XX
FA (CMB-) CAMBIA BIOSYSTEMS LLC.
XX
PI Kilian A. Bowtell D;
XX
DR WPI; 1999-106060/09.
XX
DR N-PSDB; AAX18266.
XX
FT New isolated vertebrate telomerase genes - used to develop products for
PT treating cancers or for organ regeneration; nerve cell or brain cell
PT growth following injury or bone marrow transplantation.
XX
PS Claim 4; Fig 11f-1; 134p; English.
XX
SS
CC This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of haematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful
CC in wound healing, hair growth, treatment of disease such as Wilms'
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury
XX
SQ Sequence 1132 AA;
XX
Query Match 99.7%; Score 5945; DB 2; Length 1132;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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```

QY 121 SYIPNTVTDALRGSGAMGLLRVGGDVVHLLARCALFVLVAPSCAYOCGPBLYQLGA 180
DB 121 SYIPNTVTDALRGSGAMGLLRVGGDVVHLLARCALFVLVAPSCAYOCGPBLYQLGA 180
QY 181 ATQARPPHAGSGRRRLGCEAMNHSYREAGVPLGAPAGARRGGSASRLPLPRPR 240
DB 181 ATQARPPHAGSGRRRLGCEAMNHSYREAGVPLGAPAGARRGGSASRLPLPRPR 240
QY 241 GAAPPEPRTVGGGSMHPCRTGSPDRGCVVSPAPAEALSLGALSGTHSHSPVG 300
DB 241 GAAPPEPRTVGGGSMHPCRTGSPDRGCVVSPAPAEALSLGALSGTHSHSPVG 300
QY 301 ROHHAGPSTSRPPRPWDTCPPVYAETKHFILYSGDKEQLRPSFLSLRPSLTGARL 360
DB 301 ROHHAGPSTSRPPRPWDTCPPVYAETKHFILYSGDKEQLRPSFLSLRPSLTGARL 360
QY 361 VETIFLGSRPWNMGTPRLRLPQRYWQAPFLLELIGNAQCPYGLTKTHCPPLAAYT 420
DB 361 VETIFLGSRPWNMGTPRLRLPQRYWQAPFLLELIGNAQCPYGLTKTHCPPLAAYT 420
QY 421 PAAGVCAKREKPGQSVAAPEEDTDPRRLVQLRQHSFPQVYGFVACLRPLVPGLMGS 480
DB 421 PAAGVCAKREKPGQSVAAPEEDTDPRRLVQLRQHSFPQVYGFVACLRPLVPGLMGS 480
QY 481 RHNERREFLRNTKKFISLGKHAKLSLQELTWKMSVRCAMLRSPGVGCVAASHRLREBI 540
DB 481 RHNERREFLRNTKKFISLGKHAKLSLQELTWKMSVRCAMLRSPGVGCVAASHRLREBI 540
QY 541 LAKEFLHMLSVYVVELRSFVYETETEOGNRLPEVRPSWKLQSIGRQHLKRYOLE 600
DB 541 LAKEFLHMLSVYVVELRSFVYETETEOGNRLPEVRPSWKLQSIGRQHLKRYOLE 600
QY 601 LSEAEVQHRERARPALTSRLRFLPKPDGLRPLVNMVYVVGARTFRREKAEELTSRYVA 660
DB 601 LSEAEVQHRERARPALTSRLRFLPKPDGLRPLVNMVYVVGARTFRREKAEELTSRYVA 660
QY 661 LFSVLNTERARRPQLGASVGLDDDIRAMRTFVLRRADDPPELYFVAVDTGAYDTI 720
DB 661 LFSVLNTERARRPQLGASVGLDDDIRAMRTFVLRRADDPPELYFVAVDTGAYDTI 720
QY 721 POBLTEVIAIIRKPORTYCVRRYAVVQKAAHGVKRAKFSHSTLTLDOPYKRFVANH 780
DB 721 POBLTEVIAIIRKPORTYCVRRYAVVQKAAHGVKRAKFSHSTLTLDOPYKRFVANH 780
QY 781 QETSPLRDAAVIVROSSLNEASSGLFVFLRPMCHAVRIRKGSVYOCQIPGGSILSTL 840
DB 781 QETSPLRDAAVIVROSSLNEASSGLFVFLRPMCHAVRIRKGSVYOCQIPGGSILSTL 840
QY 841 LQSLCYGDMENKLPAGIRRDGILLRLVDDPLVTPHILTHAKTFLRLTVRCPVGVVNH 900
DB 841 LQSLCYGDMENKLPAGIRRDGILLRLVDDPLVTPHILTHAKTFLRLTVRCPVGVVNH 900
QY 901 RKTIVNPFVEDEALGTAFFVQMPAHGLFPMCGILLDRITLEVQSDVSVARTSIRASLTF 960
DB 901 RKTIVNPFVEDEALGTAFFVQMPAHGLFPMCGILLDRITLEVQSDVSVARTSIRASLTF 960
QY 961 NRGKARARNRRKLPGLVRLKCHSLFLDLQVNSIQVYCNIVYKILLLOARHFACTQLCP 1020
DB 961 NRGKARARNRRKLPGLVRLKCHSLFLDLQVNSIQVYCNIVYKILLLOARHFACTQLCP 1020
QY 1021 FHQGWANPFPFLRVISDTASLQSYILKAKNAGSLGAKNAAAPLPSEAVQWMLCHQAFLL 1080
DB 1021 FHQGWANPFPFLRVISDTASLQSYILKAKNAGSLGAKNAAAPLPSEAVQWMLCHQAFLL 1080
QY 1081 KLTRHRRTVYPLJGSLRTAQTQSRKLPGLTTLTALAAANPALPSDKTILLD 1132
DB 1081 KLTRHRRTVYPLJGSLRTAQTQSRKLPGLTTLTALAAANPALPSDKTILLD 1132

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RESULT 29
AA128401
ID AA128401 standard; proceim; 1132 AA.

```

XX AC AA128401;
XX DT 22-SEP-1999 (first entry)
XX DE Human EST2 protein sequence.
XX KW EST2; proliferative capacity; cellular proliferation; decubitus ulcer;
XX KW telomerase-activating therapeutic agent; cell life-span extension;
XX KW venous disease; venous stasis ulcer; excessive pressure; arterial ulcer;
XX KW tissue regeneration enhancer; atherosclerosis; therapy.
XX OS Homo sapiens.
XX PN WO9935243-A2.
XX PD 15-JUL-1999.
XX PF 12-JAN-1999; 99WO-US000682.
XX PR 12-JAN-1998; 98US-0071220P.
XX PR 13-JAN-1998; 98US-0071455P.
XX PR 21-APR-1998; 98US-00063657.
XX PA (COLD-) COLD SPRING HARBOR LAB.
XX PI Hannon GJ, Beach DH;
XX DR WPI: 1999-444196/37.
XX DR N-P8DB; AAX89424.
XX PT Increasing proliferative capacity of cells useful for promoting wound
XX PT healing.
XX PS Claim 3; Page 65-70; 73pp; English.
XX CC This sequence is the human EST2 protein, and can be used in the method of
XX CC the invention. The method is for increasing the proliferative capacity of
XX CC cells, and comprises contacting the cell with a telomerase-activating
XX CC therapeutic agent (TAA). The method can be used for extending the life-
XX CC span of cells, e.g. by increasing the number of mitotic divisions. The
XX CC can be used for e.g. the extension of skin or other epithelial cell
XX CC cultures or grafts, the expansion of mesenchymal cell cultures or grafts,
XX CC and the expansion of chondrocyte or osteocyte cultures or grafts. They
XX CC can be applied to e.g. neuronal, haematopoietic, epithelial, pancreatic,
XX CC hepatic, chondrocytic and osteocytic stem and progenitor cells in in
XX CC vivo, in vitro or ex vivo protocols. The methods can be used for
XX CC promoting the healing of wounds resulting from e.g. surgery, burns,
XX CC inflammation or irritation or ulcers resulting from e.g. venous disease
XX CC (venous stasis ulcers), excessive pressure (decubitus ulcers) or arterial
XX CC ulcers. They can also be used to enhance tissue regeneration processes,
XX CC e.g. of the skin, hair and/or fingernails. They can also be used for
XX CC treating age-related conditions, e.g. atrophy of the skin through loss of
XX CC extracellular matrix homeostasis in dermal fibroblasts, age-related
XX CC macular degeneration caused by accumulation of lipofuscin and
XX CC downregulation of a neuronal survival factor in retinal pigmented
XX CC epithelial (RPE) cells, and atherosclerosis caused by loss of
XX CC proliferative capacity and overexpression of hypertensive and thrombotic
XX CC factors in endothelial cells. Expanded populations of normal or
XX CC genetically engineered rejuvenated cells could be used for autologous or
XX CC allogeneic cell and gene therapy. They can also be used for prolonging
XX CC the lifespan of a culture of normal cells or tissue being used to secrete
XX CC therapeutic or other commercially significant proteins and products
XX CC
XX SO Sequence 1132 AA;

```

Query Match 99.7%; Score 5945; DB 2; Length 1132;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 MPRAPRCVAVSLLSHRYEVLPATFVRRLGPGQMRVVGSDPAFAFALVAQCLVCPW 60
1 MPRAPRCVAVSLLSHRYEVLPATFVRRLGPGQMRVVGSDPAFAFALVAQCLVCPW 60

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QY 61 DAPPPAAASFQVSLKELVAVVQRLCEGAKVLAAPFLLGAGGPPPEATTSSVR 120
DB 61 DAPPPAAASFQVSLKELVAVVQRLCEGAKVLAAPFLLGAGGPPPEATTSSVR 120
QY 121 SYLENTVTDALGSGMAGLLRRVGDVVLHJLACALFVLAAPGAVQVGPPLYQGA 180
DB 121 SYLENTVTDALGSGMAGLLRRVGDVVLHJLACALFVLAAPGAVQVGPPLYQGA 180
QY 181 ATQARPPPASGPPRRRLGGERAMNHSVREAGVPLGAPAGARRGGASRSILPKRRR 240
DB 181 ATQARPPPASGPPRRRLGGERAMNHSVREAGVPLGAPAGARRGGASRSILPKRRR 240
QY 241 GAAPERTPVGSGAAHAGRTGSDRGFCVSPAPAPAEATSEGAISGRHSHPVG 300
DB 241 GAAPERTPVGSGAAHAGRTGSDRGFCVSPAPAPAEATSEGAISGRHSHPVG 300
QY 301 ROHAGPSTSPRPBWDTPCPVYATKHFYSSGDKEQLRPSFLSLSPSLTGARL 360
DB 301 ROHAGPSTSPRPBWDTPCPVYATKHFYSSGDKEQLRPSFLSLSPSLTGARL 360
QY 361 VETIFLGSRPWMPGPRRLPRLPORYQMRPLFELIGHACCPYGLKTHCPRLAVT 420
DB 361 VETIFLGSRPWMPGPRRLPRLPORYQMRPLFELIGHACCPYGLKTHCPRLAVT 420
QY 421 PAAGVCAERKPOGSAAPPEEDTDPRLVQLRHSPPVQYGFYACLRRLVPPGLWGS 480
DB 421 PAAGVCAERKPOGSAAPPEEDTDPRLVQLRHSPPVQYGFYACLRRLVPPGLWGS 480
QY 481 RHNERRFLNKKFISLGNALSLQELTKMSVYDCAMLRSPGVCPAAERLREI 540
DB 481 RHNERRFLNKKFISLGNALSLQELTKMSVYDCAMLRSPGVCPAAERLREI 540
QY 541 LAKEFLHMLSVVVELLRFYVETTTPOKNLFPYRPSVMSKOSIGIRHLKRVQRE 600
DB 541 LAKEFLHMLSVVVELLRFYVETTTPOKNLFPYRPSVMSKOSIGIRHLKRVQRE 600
QY 601 LBAEVRQREARPAALTSRLFPKPDGLPIVMDYVAGARTRRREKARLTSRYKA 660
DB 601 LBAEVRQREARPAALTSRLFPKPDGLPIVMDYVAGARTRRREKARLTSRYKA 660
QY 661 LBSVLYERARRPGLGASVGLDIDIRAMRTFVLRVAADPPPELVKADVTGAYTI 720
DB 661 LBSVLYERARRPGLGASVGLDIDIRAMRTFVLRVAADPPPELVKADVTGAYTI 720
QY 721 PODRLTEVIASIIKQNTYCVARYAVVOKAAHGRKAKFKSHVSTLTLQPMRQFVAHL 780
DB 721 PODRLTEVIASIIKQNTYCVARYAVVOKAAHGRKAKFKSHVSTLTLQPMRQFVAHL 780
QY 781 QETSPLRDAVVTFOSSSLNEASSGLFDVYLRPMCHAVIRKKSIVQCGSLPQGSILSTL 840
DB 781 QETSPLRDAVVTFOSSSLNEASSGLFDVYLRPMCHAVIRKKSIVQCGSLPQGSILSTL 840
QY 841 LQSLCYGDMENKLFAGIRRDGILLRLVDFLLVTHLTHAKTFLTLRGVPEXCVNL 900
DB 841 LQSLCYGDMENKLFAGIRRDGILLRLVDFLLVTHLTHAKTFLTLRGVPEXCVNL 900
QY 901 RCTVMPFPEDEALGTAIVQMPAGLFPWCGLLDITLLEVQSYSSYATSTRASTF 960
DB 901 RCTVMPFPEDEALGTAIVQMPAGLFPWCGLLDITLLEVQSYSSYATSTRASTF 960
QY 961 NNGFKAGRMRKLFEGVLRKCHSLFLDLQVNSLQTVCTNITYKILLDAYFFHACVLOLP 1020
DB 961 NNGFKAGRMRKLFEGVLRKCHSLFLDLQVNSLQTVCTNITYKILLDAYFFHACVLOLP 1020
QY 1021 FHQOVWKNFTFLRLVISDTASLCYSILAKAKNAGSLGKGAAGPJPSEAVOMLCHOAFL 1080
DB 1021 FHQOVWKNFTFLRLVISDTASLCYSILAKAKNAGSLGKGAAGPJPSEAVOMLCHOAFL 1080
QY 1081 KLTBRHVTVPVLGSLRTAQOTLSRKLPGTTLTALEAANPALPSDFTTIID 1132
DB 1081 KLTBRHVTVPVLGSLRTAQOTLSRKLPGTTLTALEAANPALPSDFTTIID 1132

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RESULT 30
AA96566
ID AA96566 standard; protein; 1132 AA.
XX
AC AA96566;
XX
DT 12-SEP-2000 (first entry)
XX
DE hEST2, a human telomerase catalytic subunit homologue.
XX
XX hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
XX retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
XX proliferation; immortal; tumour therapy; macular degeneration;
XX activator. INK4.
XX
OS Homo sapiens.
XX
EN W0200031238-A2.
XX
PD 02-JUN-2000.
XX
PE 24-NOV-1999; 99NO-US027907.
XX
PR 25-NOV-1998; 98US-010991P.
XX
PR 17-FEB-1999; 99US-0120549P.
XX
PA (GENE-) GENETICA INC.
XX
PI Hannon GJ, Beach DH;
XX
DR WPI; 2000-400055/34.
XX
DR N-PSDB; AAA29388.
XX
PT New method for increasing the proliferative capacity of cell lines
PT comprising administering agents reversibly activating telomerase activity
PT and reversibly inactivating Rb/INK4 and/or p53 pathways useful in
PT treating age related diseases.
XX
XX Claim 14; Page 116-119; 123pp; English.
XX
XX This protein, designated hEST2, is a human telomerase catalytic subunit
XX homologue of yeast EST2p and Euplores p123. hEST2 is a member of the
XX reverse transcriptase family of enzymes. The invention concerns methods
XX and reagents for extending the life-span, e.g. the number of mitotic
XX divisions, of a cell. The method relies on activation of a telomerase
XX activity and inhibition of one or both of a retinoblastoma (Rb)/INK4
XX pathway or a p53 pathway. Phosphorylation of Rb by cyclin-dependent
XX kinases, cdk4 and cdk6, releases the cells into the division cycle.
XX Binding of INK4 family members, e.g. the tumour suppressor p16INK4a,
XX inhibits kinase activity and results in growth arrest. Rb inactivators
XX can selectively and reversibly inactivate an Rb/INK4 pathway, especially
XX an Rb/p16INK4a pathway. The oncoprotein MDM2 is a cellular inhibitor of
XX Rb/E2F function and the p53 tumour suppressor and can also be used in the
XX methods. Other molecules which can be used include cdk4 or cdk6 mutants.
XX In particular, a cdk4 mutant is one which differs from at one or more of
XX residues K22, R24, H95 and/or D97. Additional constructs include a
XX papilloma virus E7 protein, or other viral oncoprotein which bypasses Rb
XX and/or p53. Antisense constructs of the Rb and p16INK4 genes may also be
XX used. The methods are useful for increasing the proliferative capacity of
XX cells. The cells are subsequently of use in pharmaceutical and cosmetic
XX preparations used to treat conditions related to (premature) ageing, e.g.
XX macular degeneration and arteriosclerosis. The cells can also be used to
XX replace tumour cell lines in vitro and for studies on biochemical and
XX physiological aspects of growth and differentiation. Long lived
XX (immortal) cells could also be of use in the production of normal or
XX genetically engineered biotechnology products
XX
SQ Sequence 1132 AA;

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Query Match 99.7%; Score 5945; DB 3; Length 1132;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MPRAPRCRAVSLRSHREVLPLATFVRRLGPOGMRVLVORGDPAPAFRALVACLVCPW 60
 DB 1 MPRAPRCRAVSLRSHREVLPLATFVRRLGPOGMRVLVORGDPAPAFRALVACLVCPW 60
 QY 61 DARPAPAPSPROVSCLELVARVLQRLCERGANVLAFGALLDGAARGPPEAFTTSVR 120
 DB 61 DARPAPAPSPROVSCLELVARVLQRLCERGANVLAFGALLDGAARGPPEAFTTSVR 120
 QY 121 SYLPTVTDALRGSGAMGLLRVGGDVVHLARCALFVLAAPSCAYOVGPPLYOLGA 180
 DB 121 SYLPTVTDALRGSGAMGLLRVGGDVVHLARCALFVLAAPSCAYOVGPPLYOLGA 180
 QY 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGAPGARRGGASRSPLPKRPRR 240
 DB 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGAPGARRGGASRSPLPKRPRR 240
 QY 241 GAAPBEERTPVGGSWAHPCRTGPDGRGCVVSPARPAEATSLGALSGTRHSHPSVG 300
 DB 241 GAAPBEERTPVGGSWAHPCRTGPDGRGCVVSPARPAEATSLGALSGTRHSHPSVG 300
 QY 301 RQHNAAPSTSRPPRMDPCPPVYAEKHPLYSSGDXCOLPSFLLSLRSLTGARL 360
 DB 301 RQHNAAPSTSRPPRMDPCPPVYAEKHPLYSSGDXCOLPSFLLSLRSLTGARL 360
 QY 361 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFELLLGNHAQCPYGLLKTHCPRAAVT 420
 DB 361 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFELLLGNHAQCPYGLLKTHCPRAAVT 420
 QY 421 PAAGVAREPQSSVAAPEBEDTDPRLVQLRQSHSPQVYGFVACIRLVPRLQMS 480
 DB 421 PAAGVAREPQSSVAAPEBEDTDPRLVQLRQSHSPQVYGFVACIRLVPRLQMS 480
 QY 481 RHNERFRLLRTKFFSLGKAKLSLOELTMKMSVRCAMLRSPGVCPAAEHRLREI 540
 DB 481 RHNERFRLLRTKFFSLGKAKLSLOELTMKMSVRCAMLRSPGVCPAAEHRLREI 540
 QY 541 LAFPLHMLSVVYVELLRSPFYTTETTFQKNRLEPRPSVSKLQSGIRQHKRYQRE 600
 DB 541 LAFPLHMLSVVYVELLRSPFYTTETTFQKNRLEPRPSVSKLQSGIRQHKRYQRE 600
 QY 601 LSAEVRQHRHARPALLTSLRFLPKPDGRPIVNMNDVYVGARTFRERKAERLTSRYA 660
 DB 601 LSAEVRQHRHARPALLTSLRFLPKPDGRPIVNMNDVYVGARTFRERKAERLTSRYA 660
 QY 661 LFSVLNVERARBRGLGASVLAGDIDHRAWRFLVLRQAQDPPELIFYKVDVTGAYDTI 720
 DB 661 LFSVLNVERARBRGLGASVLAGDIDHRAWRFLVLRQAQDPPELIFYKVDVTGAYDTI 720
 QY 721 PQRRLTEVLASITKPPQNTYCVRRYAVQKRAHGVKAPKSHVSTLTDIOPYMRQVVAL 780
 DB 721 PQRRLTEVLASITKPPQNTYCVRRYAVQKRAHGVKAPKSHVSTLTDIOPYMRQVVAL 780
 QY 781 QETSPLRDVAVIEQSSSLNEASSGLFDFVLFKCHHAVRIRGKSYVQCGOIPQSGSLSTL 840
 DB 781 QETSPLRDVAVIEQSSSLNEASSGLFDFVLFKCHHAVRIRGKSYVQCGOIPQSGSLSTL 840
 QY 841 LGSCLCGDNENKLPAGIRDDGLLLRVDFLVTPLTHAKTLRLTLVGVPEYGCVVNL 900
 DB 841 LGSCLCGDNENKLPAGIRDDGLLLRVDFLVTPLTHAKTLRLTLVGVPEYGCVVNL 900
 QY 901 RKVVVPPVDEALGGAFVQMPAHGFPWCGALLTRTLEVOSSDSSARTIRASVFE 960
 DB 901 RKVVVPPVDEALGGAFVQMPAHGFPWCGALLTRTLEVOSSDSSARTIRASVFE 960
 QY 961 NRGFKAQRNRRLFGVLRKCHSLFLDLQVNSLQTVCTNITYILLQAVRPACTYOLP 1020
 DB 961 NRGFKAQRNRRLFGVLRKCHSLFLDLQVNSLQTVCTNITYILLQAVRPACTYOLP 1020
 QY 1021 FHQQWKNPTEFLRVISDTSAGCSILKAKNAGMSLGAKAGAPLSEAVQOMCHOAFLL 1080
 DB 1021 FHQQWKNPTEFLRVISDTSAGCSILKAKNAGMSLGAKAGAPLSEAVQOMCHOAFLL 1080

QY 1081 KLTRHRYTVYVLLGSLRTAQTOLSRKLPGLTLLALEAANPALPSDEKTLID 1132
 DB 1081 KLTRHRYTVYVLLGSLRTAQTOLSRKLPGLTLLALEAANPALPSDEKTLID 1132

RESULT 31
 ADC47061
 ID ADC47061 standard; protein, 1132 AA.
 XX
 AC ADC47061;
 DT 18-DEC-2003 (first entry)
 XX
 DE Human TERT amino acid sequence #SEQ ID 2.
 XX
 KM Human; TERT; telomerase; antibody; reverse transcriptase; tumour;
 KM autoimmune disease; liver cancer.
 OS Homo sapiens.
 PN WO2003054545-A1.
 XX
 PD 03-JUL-2003.
 XX
 PF 19-DEC-2002; 2002WO-JP013310.
 XX
 PR 21-DEC-2001; 2001JP-00390050.
 XX
 PA (MITS-) MITSUBISHI KAGAKU MEDICAL INC.
 PA (MIRA/) MURAKAMI S.
 PA (KANE/) KANEKO S.
 PI Murakami S, Kaneko S, Masutomi K;
 XX
 DR WPI; 2003-569289/53.
 DR N-PSDB; ADC47060.
 XX
 PT Detecting anti-telomerase antibody for detecting tumors and autoimmune
 PT disease.
 XX
 PS Example Examples; Page 36-41; 45pp; Japanese.
 XX
 CC The invention relates to a method for detecting an anti-telomerase
 CC antibody. The method of the invention comprises reacting telomerase
 CC producing protein and a fragment or complex of template RNA with anti-
 CC telomerase antibody in a sample, and analysing the product. The
 CC telomerase producing protein is preferably telomerase reverse
 CC transcriptase, and the analysis method is preferably western blot. The
 CC method can also be used to detect for tumours and autoimmune disease. The
 CC method can also be used for detecting liver cancer. The current sequence
 CC represents the human TERT amino acid sequence.
 XX
 SQ Sequence 1132 AA;

Query Match 99.7%; Score 5945; DB 7; Length 1132;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVSLRSHREVLPLATFVRRLGPOGMRVLVORGDPAPAFRALVACLVCPW 60
 DB 1 MPRAPRCRAVSLRSHREVLPLATFVRRLGPOGMRVLVORGDPAPAFRALVACLVCPW 60
 QY 61 DARPAPAPSPROVSCLELVARVLQRLCERGANVLAFGALLDGAARGPPEAFTTSVR 120
 DB 61 DARPAPAPSPROVSCLELVARVLQRLCERGANVLAFGALLDGAARGPPEAFTTSVR 120
 QY 121 SYLPTVTDALRGSGAMGLLRVGGDVVHLARCALFVLAAPSCAYOVGPPLYOLGA 180
 DB 121 SYLPTVTDALRGSGAMGLLRVGGDVVHLARCALFVLAAPSCAYOVGPPLYOLGA 180
 QY 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGAPGARRGGASRSPLPKRPRR 240
 DB 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGAPGARRGGASRSPLPKRPRR 240

QY 241 GAAPERTPVGSGWAHPGRTGSDRGFCVVSAPAEATSLGALSGTRHSHPSVG 300
DB 241 GAAPERTPVGSGWAHPGRTGSDRGFCVVSAPAEATSLGALSGTRHSHPSVG 300
QY 301 RQHHAGPSTSPRPWDTPCPVVAETGFLYSSGDKQOLRPSLTLGARTL 360
DB 301 RQHHAGPSTSPRPWDTPCPVVAETGFLYSSGDKQOLRPSLTLGARTL 360
QY 361 VETIFLGSPPMGPTRRLPRLPORYMQRPLFLTLGNHACCPGLTKHCPRAV 420
DB 361 VETIFLGSPPMGPTRRLPRLPORYMQRPLFLTLGNHACCPGLTKHCPRAV 420
QY 421 PAAGVCAREKPOGSVAPEEDTDPRLVQLRHSSPMQVGFYACLRRLVPPGLMGS 480
DB 421 PAAGVCAREKPOGSVAPEEDTDPRLVQLRHSSPMQVGFYACLRRLVPPGLMGS 480
QY 481 RHNRRRLNTKKTSLGKHAQSLQELTWKMSVDCAMLRSPGVCPAAERLRREI 540
DB 481 RHNRRRLNTKKTSLGKHAQSLQELTWKMSVDCAMLRSPGVCPAAERLRREI 540
QY 541 LAKFLHMLSVYVELLSRFYVETTPQKRLFFRPSVMSKLSIGIRQHLKRVQRE 600
DB 541 LAKFLHMLSVYVELLSRFYVETTPQKRLFFRPSVMSKLSIGIRQHLKRVQRE 600
QY 601 LSEAEVROHREARPLTLRLEFIPKPGRLPIVMQDVVGAARTREKRAERLTSRYKA 660
DB 601 LSEAEVROHREARPLTLRLEFIPKPGRLPIVMQDVVGAARTREKRAERLTSRYKA 660
QY 661 LFSVINEBARRRPGLGASVGLDIDHRAMTFVLRVADPPPELVKXVDVTAAYPTI 720
DB 661 LFSVINEBARRRPGLGASVGLDIDHRAMTFVLRVADPPPELVKXVDVTAAYPTI 720
QY 721 PODRLTEVASTIKQNTYCVRRYAVVQKAAHGVKRAFKSHVSTLTLQPYMROFVAHL 780
DB 721 PODRLTEVASTIKQNTYCVRRYAVVQKAAHGVKRAFKSHVSTLTLQPYMROFVAHL 780
QY 781 QETSPRLADVIEQSSSLNEASSGLFDFELRMCHEAVIRKGSYVQCGIPQSSILSTL 840
DB 781 QETSPRLADVIEQSSSLNEASSGLFDFELRMCHEAVIRKGSYVQCGIPQSSILSTL 840
QY 841 LGSLEYGVNENKLFAGIRDDGLLRLVDFLLVTPHLLTHAKTFLTLVRGVPEYGVN 900
DB 841 LGSLEYGVNENKLFAGIRDDGLLRLVDFLLVTPHLLTHAKTFLTLVRGVPEYGVN 900
QY 901 RKTIVNPEPEDALGTAFAVQMPAHGLFPWCGLLDITLLEQSSYSYASRTSASATF 960
DB 901 RKTIVNPEPEDALGTAFAVQMPAHGLFPWCGLLDITLLEQSSYSYASRTSASATF 960
QY 961 NRGFYAGRMRRKTLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYEFHACVQLP 1020
DB 961 NRGFYAGRMRRKTLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYEFHACVQLP 1020
QY 1021 FHQQVWKNPTFFLRVISTDASLCYSLKAKAAGSLGAKGAAGPLPSAVVWLCHQAFLL 1080
DB 1021 FHQQVWKNPTFFLRVISTDASLCYSLKAKAAGSLGAKGAAGPLPSAVVWLCHQAFLL 1080
QY 1081 KLTRRRTVYVPLGSLRTAQTLQSLKLTGTLTALAEANPALPSDFITLID 1132
DB 1081 KLTRRRTVYVPLGSLRTAQTLQSLKLTGTLTALAEANPALPSDFITLID 1132
RESULT 32
ADE40482
ID ADE40482 standard; protein; 1132 AA.
XX
XX
AC ADE40482;
XX
XX 29-JAN-2004 (first entry)
DE Human telomerase reverse transcriptase (hTERT).
XX
XX Immortal porcine cell; telomerase reverse transcriptase; epithelial cell;
KW

KM uterine endometrial glandular tissue; virus quantification;
KW virus production; porcine reproductive and respiratory syndrome virus;
KM PRRSV; toxicity evaluation; human; hTERT; enzyme.
XX
XX Hemo sapiens.
XX
XX W0203077853-A2.
XX
XX 25-SEP-2003.
XX
XX 11-MAR-2003; 2003MO-US007526.
XX
XX 11-MAR-2002; 2002US-0363129P.
XX
XX (MINTU) UNIV MINNESOTA.
XX
XX Farris UA, Foster DN, O'Grady SM;
XX
XX WPI: 2003-779075/73.
XX
XX N-PSDB; ADE40481.
XX
XX New immortal porcine cell comprising a polynucleotide encoding an
XX PT exogenous telomerase reverse transcriptase polypeptide, useful for
XX PT measuring the amount of virus in a sample or for evaluating toxicity of a
XX PT compound.
XX
XX Claim 4; SEQ ID NO 2; 42DP; English.
XX
XX The invention relates to immortal porcine cells comprising a
XX CC polynucleotide encoding an exogenous telomerase reverse transcriptase
XX CC (hTERT). The invention also encompasses the method of making immortal
XX CC porcine cells, and the use of the immortal porcine cells for measuring
XX CC the amount of virus in a sample, producing a virus, and evaluating the
XX CC toxicity of a compound. The cells of the invention may be diploid or
XX CC aneuploid, and may be an epithelial cell obtained from uterine
XX CC endometrial glandular tissue. The exogenous telomerase reverse
XX CC transcriptase expressed by the cells of the invention is preferably human
XX CC telomerase reverse transcriptase (ADE40482). The immortal porcine cells
XX CC are useful for measuring an amount of a virus in a sample, producing a
XX CC virus (especially porcine reproductive and respiratory syndrome virus
XX CC (PRRSV)), or for evaluating toxicity of a compound. The present sequence
XX CC represents human telomerase reverse transcriptase (hTERT), which is
XX CC claimed for use in the immortal cells of the invention.
SQ Sequence 1132 AA;
Query Match 99.7%; Score 5945; DB 7; Length 1132;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1129; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSILSHYREVLPATFVRLPQCGRLVQRGDPAFALVACLVCFW 50
DB 1 MPAPRCRAVRSILSHYREVLPATFVRLPQCGRLVQRGDPAFALVACLVCFW 50
QY 61 DAPPPAPSPFQVSCLEKLVAVVYLQRCERAKVLAFGFALLDQARGPPEARTTSVR 120
DB 61 DAPPPAPSPFQVSCLEKLVAVVYLQRCERAKVLAFGFALLDQARGPPEARTTSVR 120
QY 121 SYLPNTVTALRGSGAMGILLRRVGDVYVHLLARCAFLVAVPSCAYOVGCPPLXOLGA 180
DB 121 SYLPNTVTALRGSGAMGILLRRVGDVYVHLLARCAFLVAVPSCAYOVGCPPLXOLGA 180
QY 181 ATQARPPPHAGSRRRLGCERAMNHSVREAGVPLGLPAGARRGSGASRLPLKRPBR 240
DB 181 ATQARPPPHAGSRRRLGCERAMNHSVREAGVPLGLPAGARRGSGASRLPLKRPBR 240
QY 241 GAAPERTPVGSGWAHPGRTGSDRGFCVVSAPAEATSLGALSGTRHSHPSVG 300
DB 241 GAAPERTPVGSGWAHPGRTGSDRGFCVVSAPAEATSLGALSGTRHSHPSVG 300
QY 301 RQHHAGPSTSPRPWDTPCPVVAETGFLYSSGDKQOLRPSLTLGARTL 360
DB 301 RQHHAGPSTSPRPWDTPCPVVAETGFLYSSGDKQOLRPSLTLGARTL 360

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QY 361 VETIFGSRPMPGCTPRRLPRLPQRYWQMPLELLELGNHACQPYVLLKTHCPLRAAVT 420
DB 361 VETIFGSRPMPGCTPRRLPRLPQRYWQMPLELLELGNHACQPYVLLKTHCPLRAAVT 420
QY 421 PAAGVACREKPGQSVAAPEEDTDPRLVOLLKQHSPPQVYGFVACLRVLPGLMGS 480
DB 421 PAAGVACREKPGQSVAAPEEDTDPRLVOLLKQHSPPQVYGFVACLRVLPGLMGS 480
QY 481 RHNERFRLNTKTKFISLGKAKLSLOELTWKMSVRCAMLRSPGVCYPAAEHRLRETI 540
DB 481 RHNERFRLNTKTKFISLGKAKLSLOELTWKMSVRCAMLRSPGVCYPAAEHRLRETI 540
QY 541 LAKEFLMWSVYVVELLRSEFFYTETTFQKNRLFFYRKSVMKLSQSIGRQHKRYQJRE 600
DB 541 LAKEFLMWSVYVVELLRSEFFYTETTFQKNRLFFYRKSVMKLSQSIGRQHKRYQJRE 600
QY 601 LSEAEVRQREAPALITSRIRPKDGLRPIVNDYVVGATFEREKRAELTSRYKA 660
DB 601 LSEAEVRQREAPALITSRIRPKDGLRPIVNDYVVGATFEREKRAELTSRYKA 660
QY 661 LSEAEVRQREAPALITSRIRPKDGLRPIVNDYVVGATFEREKRAELTSRYKA 660
DB 661 LSEAEVRQREAPALITSRIRPKDGLRPIVNDYVVGATFEREKRAELTSRYKA 660
QY 721 PODRLTEVLASIIKPNQTVCRRYAVVQKAAHGVKAKFASHVSLTDLQPYMRQFAHL 780
DB 721 PODRLTEVLASIIKPNQTVCRRYAVVQKAAHGVKAKFASHVSLTDLQPYMRQFAHL 780
QY 781 QETSPYRDVAVITQSSSLNBAASGLFDVFLRFMCHNAVRIRKSYQCCGIPQGSILSTL 840
DB 781 QETSPYRDVAVITQSSSLNBAASGLFDVFLRFMCHNAVRIRKSYQCCGIPQGSILSTL 840
QY 841 LCLSLCGDMENKLFAGIRRDGLLLRLVDDPLVTPHLLTAKTFLRTLVAGVEYGVNLT 900
DB 841 LCLSLCGDMENKLFAGIRRDGLLLRLVDDPLVTPHLLTAKTFLRTLVAGVEYGVNLT 900
QY 901 RKTVPNPFVEDEALGCTAFYQMPAHGLFPWCGILLDTRTLEVQSDYSYARISIRASVT 960
DB 901 RKTVPNPFVEDEALGCTAFYQMPAHGLFPWCGILLDTRTLEVQSDYSYARISIRASVT 960
QY 961 NRGFKAGMMRRKLFVYLRLKCHSLFLDQVNSLQVNCNITVYLLLLQYRHACVLCQHP 1020
DB 961 NRGFKAGMMRRKLFVYLRLKCHSLFLDQVNSLQVNCNITVYLLLLQYRHACVLCQHP 1020
QY 1021 FHQQVKNPFFLRVISTDASLCLSYLLKAKNAGMSLGAGAGPLPSEAVQWLCHQAFLL 1080
DB 1021 FHQQVKNPFFLRVISTDASLCLSYLLKAKNAGMSLGAGAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTRHAVTVYPLIGSLRTAQTQSLKTLPGTTLTALAANPALPSPFKTILLD 1132
DB 1081 KLTRHAVTVYPLIGSLRTAQTQSLKTLPGTTLTALAANPALPSPFKTILLD 1132
QY 1081 KLTRHAVTVYPLIGSLRTAQTQSLKTLPGTTLTALAANPALPSPFKTILLD 1132
DB 1081 KLTRHAVTVYPLIGSLRTAQTQSLKTLPGTTLTALAANPALPSPFKTILLD 1132

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RESULT 33
AAM56101
ID AAM56101 standard; protein; 1405 AA.
XX
XX AAM56101;
AC
XX
XX 13-AUG-1998 (first entry)
DT
XX
DE Enhanced green fluorescent protein and hTERT fusion protein.
XX
XX Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;
XX cell proliferation; cancer; ageing; ribonucleoprotein.
OS
XX Synthetic.
XX Homo sapiens.
FH
XX Key Location/Qualifiers
FT Region 1..250
/notes="enhanced green fluorescent protein fragment"

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FT Region 276..1405
FT /note="hTERT protein fragment"
XX
XX GB2317891-A.
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
XX 18-APR-1997; 97US-00844419.
XX 25-APR-1997; 97US-00846017.
XX 06-MAY-1997; 97US-00851843.
XX 09-MAY-1997; 97US-00854050.
XX 14-AUG-1997; 97US-00811312.
XX 14-AUG-1997; 97US-00812251.
XX 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERO CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cecchi TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
XX Andrews WH;
XX WPI, 1998-171633/16.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variants - are useful in the diagnosis, prognosis and treatment of cell
XX proliferation conditions especially cancer and ageing.
XX
XX Example 15, Page 269-270; 387pp; English.
XX
XX The present sequence represents a fusion protein from an example of the
XX present invention which describes human telomerase reverse transcriptase
XX (hTERT). The present invention also describes the following methods: (A)
XX determining whether a test compound is a modulator of hTERT by detecting
XX the change in hTERT recombinant protein or polynucleotide, on
XX administration of the compound; (B) preparation of recombinant telomerase
XX by contacting a protein preparation of hTERT with a telomerase RNA
XX component; (C) detection of the hTERT RNA or protein in a sample by
XX binding a relevant probe to the sample and detecting the complex formed
XX or in the case of RNA detection, amplifying the product and correlating
XX the presence of complex or amplification product with presence of hTERT in
XX the sample; and (D) increasing the proliferation of a vertebrate cell by
XX increasing hTERT expression; and (E) the use of an agent that causes an
XX increase in cell vertebrate cell proliferation to create a medicament
XX that inhibits ageing. A protein preparation of hTERT and the
XX polynucleotide encoding hTERT can be used in the manufacture of
XX medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
XX telomerase activity can be used to treat conditions that are associated
XX with high telomerase activity. A protein preparation of hTERT can also be
XX used in the new methods
XX
XX Sequence 1405 AA:
SQ
XX
XX Query Match 99.4%; Score 5929; DB 2; Length 1405;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 1130; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
XX
XX 1 MPRAPRCAVNSLRSHYREVLPATFVRRLPGQMRLLVQGRDPAFAFALVAQGLVCVPM 60
XX 276 MPRAPRCAVNSLRSHYREVLPATFVRRLPGQMRLLVQGRDPAFAFALVAQGLVCVPM 335
XX
XX 61 DARPPAPASFRQVSCLELYARVLCGLCERGANVLAFGALLDGAAGGPPFAFTSVR 120
XX 336 DARPPAPASFRQVSCLELYARVLCGLCERGANVLAFGALLDGAAGGPPFAFTSVR 395
XX
XX 121 SYLNTVTDALRGSGAGGLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLVYOLGA 180
XX 396 SYLNTVTDALRGSGAGGLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLVYOLGA 455
XX
XX 181 ATQARPPPHASGPRRLRGCEPAMNHSYREAGVPLGLPAPGARRRGSGASSLPAPKPRR 240
XX

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DB 456 ATQASPPHAGSPRRRLGGERAMNHSVBAGVPLGLPAAGARRRGGASRSRLPPKERR 515
 QY 241 GAAPERTPVGGQSWAHGRTGSPDRGFCVSPAPAEATSLGALSGTRSHSPVG 300
 DB 516 GAAPERTPVGGQSWAHGRTGSPDRGFCVSPAPAEATSLGALSGTRSHSPVG 575
 QY 301 ROHAGPSTSPPPWPTCPVYAEKHFVYSSGDYQURPSFLSLSPSLTGARL 360
 DB 576 ROHAGPSTSPPPWPTCPVYAEKHFVYSSGDYQURPSFLSLSPSLTGARL 634
 QY 361 VETIFGSPWMPGTPRRLPRLPORYWOMRPLFELLNHAGCPYGLTKHCPRAAVT 420
 DB 635 VETIFGSPWMPGTPRRLPRLPORYWOMRPLFELLNHAGCPYGLTKHCPRAAVT 694
 QY 421 PAAGVAREKPGQSVAAPEEDTDPRLVOLLRQSSPMOYGYFVACLRRLVPGMG 480
 DB 695 PAAGVAREKPGQSVAAPEEDTDPRLVOLLRQSSPMOYGYFVACLRRLVPGMG 754
 QY 481 RHNERFRLNTKFFSLGHAHLSQELTWKMSVDCAMLRSPGVGPAARELREI 540
 DB 755 RHNERFRLNTKFFSLGHAHLSQELTWKMSVDCAMLRSPGVGPAARELREI 814
 QY 541 LAKFLHMLSVYVVELLSFFVYETTFQKNLFFYRPSVMSKQSIGIRHLRVOLRE 600
 DB 815 LAKFLHMLSVYVVELLSFFVYETTFQKNLFFYRPSVMSKQSIGIRHLRVOLRE 874
 QY 601 LSEAVRQREARAPALLTSRLFIKPDGLPIVMDYVVGARTPRKRAERLTSYKA 660
 DB 875 LSEAVRQREARAPALLTSRLFIKPDGLPIVMDYVVGARTPRKRAERLTSYKA 934
 QY 661 LPSVNTYERARRPGLGASVGLDDIHRAMRTFVRAVADPPPELVKVDYGAVDI 720
 DB 935 LPSVNTYERARRPGLGASVGLDDIHRAMRTFVRAVADPPPELVKVDYGAVDI 994
 QY 721 PODRLTEVIAIIKQNTYCVARYAVQKAAGHVRKAFKSHVSTLIDLPYMRQVANH 780
 DB 995 PODRLTEVIAIIKQNTYCVARYAVQKAAGHVRKAFKSHVSTLIDLPYMRQVANH 1054
 QY 781 QSTSPRDVYVEOSSSINENASSGLFDFELRPMCHAVRIGKSVYQCGIPOGSIISTL 840
 DB 1055 QSTSPRDVYVEOSSSINENASSGLFDFELRPMCHAVRIGKSVYQCGIPOGSIISTL 1114
 QY 841 LCLSGYGMENKLFAGIRRDGLLRLVDFLLVPHLTHAKFTLTVRVGVEXGVYVL 900
 DB 1115 LCLSGYGMENKLFAGIRRDGLLRLVDFLLVPHLTHAKFTLTVRVGVEXGVYVL 1174
 QY 901 RKTVMNFPVEDALGDTAFVQVPAHGLFPMWGLLIDRTLBYQSYSTASTIRASTVF 960
 DB 1175 RKTVMNFPVEDALGDTAFVQVPAHGLFPMWGLLIDRTLBYQSYSTASTIRASTVF 1234
 QY 961 NRGFKAGRMRRKLFGLVTLKCHSFLDQVNSLQTVCTNIYKILLQAYFFHACVQLP 1020
 DB 1235 NRGFKAGRMRRKLFGLVTLKCHSFLDQVNSLQTVCTNIYKILLQAYFFHACVQLP 1294
 QY 1021 FHQGVKNEFTFLRYISDTASLCYSILKAKNAGSLGAKGAAGLPSEAVOMLCHQAFLL 1080
 DB 1295 FHQGVKNEFTFLRYISDTASLCYSILKAKNAGSLGAKGAAGLPSEAVOMLCHQAFLL 1354
 QY 1081 KLTRRVTVVPLGLSRLTQOTLSRKLPGTTLTALEAANPALPSDFETIID 1132
 DB 1355 KLTRRVTVVPLGLSRLTQOTLSRKLPGTTLTALEAANPALPSDFETIID 1405

RESULT 34
 ID AAY00647
 AAY00647 standard; protein; 1166 AA.
 AC AAY00647;
 XX
 DT 26-JUL-1999 (first entry)
 XX
 DE Telomerase (ver. 2) protein sequence.
 XX

KM Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KM neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KM smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KM stem cell differentiation; organ regeneration; organ differentiation.
 OS Homo sapiens.
 OS Synthetic.
 PN WO9901560-A1.
 XX
 PD 14-JAN-1999.
 XX
 PF 01-JUL-1998; 98MO-US013635.
 XX
 PR 01-JUL-1997; 97US-0051410P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053329P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX
 PA (CAMP-) CAMBIA BIOSYSTEMS LLC.
 XX
 PI Kilian A. Bowtell D;
 XX
 DR WPI: 1999-106060/09.
 DR N-PDB; AAX18275.
 XX
 PT New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX
 PS Claim 4; Fig 11z-ac; 134pp; English.
 XX
 CC This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilms'
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury
 XX
 SQ Sequence 1166 AA;
 Query Match 99.2%; Score 5918; DB 2; Length 1166;
 Best Local Similarity 96.8%; Pred. No. 0;
 Matches 1129; Conservative 1; Mismatches 2; Indels 34; Gaps 1;
 QY 1 MPAPRCRAVRSLLRSHREYVPLAFVFRRLPGQGRVLVQRDDPAFRVLVAQCIVCVW 60
 DB 1 MPAPRCRAVRSLLRSHREYVPLAFVFRRLPGQGRVLVQRDDPAFRVLVAQCIVCVW 60
 QY 61 DARPAPAAASFRVY-----SCLKELVAVYLQ 86
 DB 61 DARPAPAAASFRVYGLPGVAVLGLRAAGNQRHAESSAGDSGRPRRSCLKELVAVYLQ 120
 QY 87 RICERGAKNVLAFGFALLDGAAGCPPEAFTTSVRSYLPVTVDALRGSGAMGLLRRVGD 146
 DB 121 RICERGAKNVLAFGFALLDGAAGCPPEAFTTSVRSYLPVTVDALRGSGAMGLLRRVGD 180
 QY 147 DVLVHLARCALFVLVAPSCAYOVGPPLYOIGAATQARPFAHAGSPRRRLGGERAMNHS 206
 DB 181 DVLVHLARCALFVLVAPSCAYOVGPPLYOIGAATQARPFAHAGSPRRRLGGERAMNHS 240
 QY 207 VRAGVPLGLPAPGARRGGSASRSLLPDKRRRGAAPEERTPVGGQSWAHGRTGSPS 266
 DB 241 VRAGVPLGLPAPGARRGGSASRSLLPDKRRRGAAPEERTPVGGQSWAHGRTGSPS 300

QY 120 RSYLPTVTADLRSGAWGLLRVGVDDVYLHLLARCALFVLVAESCAVYVCGPEPLYQ 179
 DB 189 RSYLPTVTADLRSGAWGLLRVGVDDVYLHLLARCALFVLVAESCAVYVCGPEPLYQ 248
 QY 180 AATQARPPPHASGPPRRRLGGERAMNHSVREAGVPLGLPAPGARRRGSASLSLPPKPR 239
 DB 249 AATQARPPPHASGPPRRRLGGERAMNHSVREAGVPLGLPAPGARRRGSASLSLPPKPR 308
 QY 240 RGAAPERTPVQGSMAHPGRTGSPDRGFCVSPAPPAEATSLEGALSGTRSHPSV 299
 DB 309 RGAAPERTPVQGSMAHPGRTGSPDRGFCVSPAPPAEATSLEGALSGTRSHPSV 368
 QY 300 GRGHAGPSTSRPRPMDTCCPPYAEKHFLLYSSGGEQRLRPSFLLSLRPLTGARR 359
 DB 369 GRGHAGPSTSRPRPMDTCCPPYAEKHFLLYSSGGEQRLRPSFLLSLRPLTGARR 428
 QY 360 LVEETIFLSGRPMMPGTPRRLPRLPORVYOMRPLFELLGNHAOCYGVLLKTHCEPLAAV 419
 DB 429 LVEETIFLSGRPMMPGTPRRLPRLPORVYOMRPLFELLGNHAOCYGVLLKTHCEPLAAV 488
 QY 420 TPAAGVCAEKPQGSVAAPBEEDTDPRLVOLLRQHSWPYVGVRACLRLVPPGLWG 479
 DB 489 TPAAGVCAEKM-QGSVAAPBEEDTDPRLVOLLRQHSWPYVGVRACLRLVPPGLWG 547
 QY 480 SHNERRPLRNTKPFISLGGHAKLSLOELTWKMSVRDCAMLRSPGVSCVPAAEHRLREE 539
 DB 548 SHNERRPLRNTKPFISLGGHAKLSLOELTWKMSVRDCAMLRSPGVSCVPAAEHRLREE 607
 QY 540 ILAKFLHMLMSVYVELLSFFVYETTFQKNRLFYRPSVWSKLSIGIRQHLKRVQLR 599
 DB 608 ILAKFLHMLMSVYVELLSFFVYETTFQKNRLFYRPSVWSKLSIGIRQHLKRVQLR 667
 QY 600 ELSEAEVRORRRARPAALLTSRLRFLPKRPGLEPIYMMYVVGARFRREKXAERLTSSVK 659
 DB 668 ELSEAEVRORRRARPAALLTSRLRFLPKRPGLEPIYMMYVVGARFRREKXAERLTSSVK 727
 QY 660 ALFSLVNTERRARPGILGASVGLDDIHRAMRTFVLARAODPPELTFVAVDVTGAYDT 719
 DB 728 ALFSLVNTERRARPGILGASVGLDDIHRAMRTFVLARAODPPELTFVAVDVTGAYDT 787
 QY 720 IPQDRITVYIASITIKPONTYCVRRYAVVOKAAGHVRKAFKSHVSTLTDLOPYMKQFVAH 779
 DB 788 IPQDRITVYIASITIKPONTYCVRRYAVVOKAAGHVRKAFKSHVSTLTDLOPYMKQFVAH 847
 QY 780 LOETSPILDAVYIEOSSSLNEASGLFVFLRFMCHAVRIRGKSYVCCGIPGOSILST 839
 DB 848 LOETSPILDAVYIEOSSSLNEASGLFVFLRFMCHAVRIRGKSYVCCGIPGOSILST 907
 QY 840 LLOSLCYGMENKLPAGIRRDGLLRVDDFLVTPHAKTFLRTLVKGVPRYGCYVN 899
 DB 908 LLOSLCYGMENKLPAGIRRDGLLRVDDFLVTPHAKTFLRTLVKGVPRYGCYVN 967
 QY 900 LKRTVVPFVEDEALGCTAFVQMPAHGLFPMCGLLDRTLEVOGDSYVARTSIRASVT 959
 DB 968 LKRTVVPFVEDEALGCTAFVQMPAHGLFPMCGLLDRTLEVOGDSYVARTSIRASVT 1027
 QY 960 FNRGFAGNMRKLEGVLRKXCHSLFDLDQVNSLQVCTNLYKILLQAVRFAACVLQL 1019
 DB 1028 FNRGFAGNMRKLEGVLRKXCHSLFDLDQVNSLQVCTNLYKILLQAVRFAACVLQL 1087
 QY 1020 PHQGVWKPPTFFLRVISTASLCSILKAKNAGSLAKGAAGLSEBAVQMCHQAF 1079
 DB 1088 PHQGVWKPPTFFLRVISTASLCSILKAKNAGSLAKGAAGLSEBAVQMCHQAF 1147
 QY 1080 LKLTRHRYVYVLLGSLRTAQTOLSRKLPCTTLTLEAANPALSPDKTILD 1132
 DB 1148 LKLTRHRYVYVLLGSLRTAQTOLSRKLPCTTLTLEAANPALSPDKTILD 1199

RESULT 36
 AAY00641
 ID AAY00641 standard; protein; 1120 AA.
 XX

AC AAY00641;
 XX
 DT 26-JUL-1999 (first entry)
 XX
 DE Telomerase protein sequence lacking motif A.
 XX
 KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN W09901560-A1.
 XX
 PD 14-JAN-1999.
 XX
 PF 01-JUL-1998; 98MO-US013835.
 XX
 PR 01-JUL-1997; 97US-0051410P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053329P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX
 PA (CAMP-) CAMBIA BIOSYSTEMS LLC.
 XX
 PI Killian A, Bowtell D,
 XX
 DR WPI; 1999-106060/09.
 DR N-PSDB; AAX18269.
 XX
 PT New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX
 PS Claim 4; Fig 11n-o; 134bp; English.
 XX
 CC This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilms'
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury
 CC
 XX
 SQ Sequence 1120 AA;
 Query Match 98.5%; Score 5873; DB 2; Length 1120;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1118; Conservative 1; Mismatches 1; Indels 12; Gaps 1;
 QY 1 MPARPCRAVRSILRSHYREVLPATFVRRLIGQGRMLVORGPPAFAFRLVQCLCVPM 60
 DB 1 MPARPCRAVRSILRSHYREVLPATFVRRLIGQGRMLVORGPPAFAFRLVQCLCVPM 60
 QY 61 DARPAPAPSPFVQSCLEKELVAVLQRLCEGAKNYLAFGALLDQARGGPEAFTTSVR 120
 DB 61 DARPAPAPSPFVQSCLEKELVAVLQRLCEGAKNYLAFGALLDQARGGPEAFTTSVR 120
 QY 121 SYLPNTVTADLRSGAWGLLRVGVDDVYLHLLARCALFVLVAESCAVYVCGPEPLYQLGA 180
 DB 121 SYLPNTVTADLRSGAWGLLRVGVDDVYLHLLARCALFVLVAESCAVYVCGPEPLYQLGA 180
 QY 181 AATQARPPPHASGPPRRRLGGERAMNHSVREAGVPLGLPAPGARRRGSASLSLPPKPRR 240

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Db      181  ATQARPPPHASGPRRRRCGERAMNHSVREAGVPLGLAPAPARRRGASASLPLPRRPR 240
Qy      241  GAAPERTPTVGGGSAHMPGRTGSPDRGCVVSPAPAEATSLGALSSTHSPSVG 300
Db      241  GAAPERTPTVGGGSAHMPGRTGSPDRGCVVSPAPAEATSLGALSSTHSPSVG 300
Qy      301  RQHAGSPSTSRPRPMDTCPPIYAEETKFKLVSSGGKEQLRPSFLSSRPSLTGARRL 360
Db      301  RQHAGSPSTSRPRPMDTCPPIYAEETKFKLVSSGGKEQLRPSFLSSRPSLTGARRL 360
Qy      361  VETIFLGSRPMPGTPRRLPLRPLQRYWQMRPLFLELLGNHAGCPYGVLLKTHCPRAAYT 420
Db      361  VETIFLGSRPMPGTPRRLPLRPLQRYWQMRPLFLELLGNHAGCPYGVLLKTHCPRAAYT 420
Qy      421  PAAGVCAKREKPGQSVAAPEEDDPRLVOLLRQHSPPMGVGFVACLRILVPGMG 480
Db      421  PAAGVCAKREKPGQSVAAPEEDDPRLVOLLRQHSPPMGVGFVACLRILVPGMG 480
Qy      481  RHNERREPLRNTKFTSLGKAHAKLSLOELTWKMSVDRDAMLRSPGVGCVAPAEHRLREEL 540
Db      481  RHNERREPLRNTKFTSLGKAHAKLSLOELTWKMSVDRDAMLRSPGVGCVAPAEHRLREEL 540
Qy      541  LAKFLHMLMSVYVELLRSEFYVTEETFGQNRLEFFRPSVSKLQSIGRQHLKRYQLRE 600
Db      541  LAKFLHMLMSVYVELLRSEFYVTEETFGQNRLEFFRPSVSKLQSIGRQHLKRYQLRE 600
Qy      601  LSEAEVQHRREARPAALITSLRFLRFPKPDGLRPIVNMDDVVGARTPREKAEELTGRVRA 660
Db      601  LSEAEVQHRREARPAALITSLRFLRFPKPDGLRPIVNMDDVVGARTPREKAEELTGRVRA 660
Qy      661  LFSVLNTERARRRPLGLGASVGLDDIHRAMRTFVLRRADPPPELTVKVDVTAAYDTI 720
Db      661  LFSVLNTERARRRPLGLGASVGLDDIHRAMRTFVLRRADPPPELTVKVDVTAAYDTI 720
Qy      721  PODRLTEVIAIITKPMNTVCVRBYAVVQKAHGHVKAFFKSHVSTLTDIQPMRQFVAHL 780
Db      721  PODRLTEVIAIITKPMNTVCVRBYAVVQKAHGHVKAFFKSHVSTLTDIQPMRQFVAHL 780
Qy      781  QETSPLADAVIIOSSSLNEASSGLPDVFLRFMCHNAVRIRGKSYVQCGIPQGSILSTL 840
Db      781  QETSPLADAVIIOSSSLNEASSGLPDVFLRFMCHNAVRIRGKSYVQCGIPQGSILSTL 840
Qy      841  LGLCLCGDMENKLPAGIRBDGLLRIVDDDLVTPHHTAKTLRLTVNGVPEYGVNVL 900
Db      841  LGLCLCGDMENKLPAGIRBDGLLRIVDDDLVTPHHTAKTLRLTVNGVPEYGVNVL 900
Qy      901  RKTVMNPFVDEALGTAFAVQMPAHGLFPCGILLDRTLEVOSSYARTSIRASVTF 960
Db      889  RKTVMNPFVDEALGTAFAVQMPAHGLFPCGILLDRTLEVOSSYARTSIRASVTF 948
Qy      961  NRGFKAGRNRRKLPFVLRKCHSLFLDLQVNSLQVTCNIVYILLQAYRFHACVQLP 1020
Db      949  NRGFKAGRNRRKLPFVLRKCHSLFLDLQVNSLQVTCNIVYILLQAYRFHACVQLP 1008
Qy      1021  FHQVWKNPTFFLRVISTDTASLCYSILKAKNAGMSLGAKAAGPLLSEAVOMLCHQAFLL 1080
Db      1009  FHQVWKNPTFFLRVISTDTASLCYSILKAKNAGMSLGAKAAGPLLSEAVOMLCHQAFLL 1068
Qy      1081  KLTRHRTVYVPLGSLRTAQTQSLRKLPGTTLTALBAANPALPSPDKTILD 1132
Db      1069  KLTRHRTVYVPLGSLRTAQTQSLRKLPGTTLTALBAANPALPSPDKTILD 1120

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RESULT 37
AA100650
ID  AA100650 standard; protein; 1120 AA.
XX
AC  AA100650;
XX
DT  26-JUL-1999 (first entry)
XX
DE  Telomerase (ver. 2) protein sequence lacking motif A.

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XX      XX      Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW      KW      neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW      KW      smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
KW      KW      stem cell differentiation; organ regeneration; organ differentiation.
OS      OS      Homo sapiens.
OS      OS      Synthetic.
XX      XX      W09501560-A1.
XX      XX      14-JAN-1999.
XX      XX      01-JUL-1998; 98MO-US013835.
XX      XX      01-JUL-1997; 97US-0054410P.
XX      XX      21-JUL-1997; 97US-0053018P.
XX      XX      21-JUL-1997; 97US-0053329P.
XX      XX      04-AUG-1997; 97US-0054642P.
XX      XX      09-SEP-1997; 97US-0058287P.
XX      XX      (CMB-) CAMBIA BIOSYSTEMS LLC.
XX      XX      Kilian A, Bowtell D,
XX      XX      WPI; 1999-106060/09.
XX      XX      DR N-PSDB; AAX18278.
XX      XX      New isolated vertebrate telomerase genes - used to develop products for
PT      PT      treating cancers or for organ regeneration, nerve cell or brain cell
XX      XX      growth following injury or bone marrow transplantation.
XX      XX      Claim 4; Fig 11ah-aj; 134p; English.
XX      XX
CC      CC      This sequence is a truncated human telomerase of the invention. Primers
CC      CC      that amplify the telomerase coding sequence can be used in a method for
CC      CC      diagnosing cancer in a patient. The telomerase can be used for detection,
CC      CC      diagnosis and drug screening. Inhibitors of telomerase activity can be
CC      CC      used to treat cancers such as melanomas, other skin cancers,
CC      CC      neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
CC      CC      lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC      CC      growth. Enhancers of telomerase may be used to stimulate stem cell
CC      CC      proliferation and differentiation (expansion of hematopoietic stem cells
CC      CC      could be administered in the bone marrow transplant context). As well,
CC      CC      many tissues have stem cells. Proliferation of these cells may be useful
CC      CC      in wound healing, hair growth, treatment of disease such as Wilms'
CC      CC      tumour, organ regeneration or differentiation after injury or diseases,
CC      CC      nerve cell or brain cell growth following injury. Note: The N-terminus of
CC      CC      this sequence can be replaced by the sequences shown in AA100656-100658
XX      XX
SQ      Sequence 1120 AA:

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Query Match      98.3%; Score 5864; DB 2; Length 1120;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 117; Conservative 1; Mismatches 2; Indels 12; Gaps 1;

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Qy      1  MPARARCAVAVSLRSHREVLPATFVRRLGPGMGLVYQGDPAARFALVAQCLVCPW 60
Db      1  MPARARCAVAVSLRSHREVLPATFVRRLGPGMGLVYQGDPAARFALVAQCLVCPW 60
Qy      61  DARPPAPSPROYSCLELVARVLRCLCEGAKNVAFGALLDGAAGGPPFAFTTSVR 120
Db      61  DARPPAPSPROYSCLELVARVLRCLCEGAKNVAFGALLDGAAGGPPFAFTTSVR 120
Qy      121  SYLPNTVTDALRGSGAWGLLRVGGDVLVHLRACALFVAVASCAVYQVGPPLVQLGA 180
Db      121  SYLPNTVTDALRGSGAWGLLRVGGDVLVHLRACALFVAVASCAVYQVGPPLVQLGA 180
Qy      181  ATQARPPPHASGPRRRRCGERAMNHSVREAGVPLGLAPAPARRRGASASLPLPRR 240
Db      181  ATQARPPPHASGPRRRRCGERAMNHSVREAGVPLGLAPAPARRRGASASLPLPRR 240
Qy      241  GAAPERTPTVGGGSAHMPGRTGSPDRGCVVSPAPAEATSLGALSSTHSPSVG 300

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Db      241 GAAPPERPFPVGGSHARGTRGSDGFCVVSAPRAAEATSTEGALSTGRSHBVG 300
Qy      301 RQHHAGPSTSPRPFRWDTCPVYAETKHLFYSSGDYEQLRPSLILSLRPSLTGARRL 360
Db      301 RQHHAGPSTSPRPFRWDTCPVYAETKHLFYSSGDYEQLRPSLILSLRPSLTGARRL 360
Qy      361 VETIFLGSPPWMPGTPRLPRLPQRYWQRPFLFELGNHACCPYGLKTHCPRAVLT 420
Db      361 VETIFLGSPPWMPGTPRLPRLPQRYWQRPFLFELGNHACCPYGLKTHCPRAVLT 420
Qy      421 PAAGVAREKPOGSAVAPEEDTDPRLVQLRHSSPMOYGFYRACLRLVPPGLWGS 480
Db      421 PAAGVAREKPOGSAVAPEEDTDPRLVQLRHSSPMOYGFYRACLRLVPPGLWGS 480
Qy      481 RHNERFLNTRKFLISLGHAKLSLOELTWKMSVDCAMLRSPGVGVPAEHLREI 540
Db      481 RHNERFLNTRKFLISLGHAKLSLOELTWKMSVDCAMLRSPGVGVPAEHLREI 540
Qy      541 LAKEJHMLSVYVELLRSFYVETTFPOKRLFPYRPSVSKLOSIGRQHLKRVQRE 600
Db      541 LAKEJHMLSVYVELLRSFYVETTFPOKRLFPYRPSVSKLOSIGRQHLKRVQRE 600
Qy      601 LSEAEVQRHREARPALITSLRFLPKPGCLPIVNMVYVAGARTREKAEHLTSRYKA 660
Db      601 LSEAEVQRHREARPALITSLRFLPKPGCLPIVNMVYVAGARTREKAEHLTSRYKA 660
Qy      661 LFSVLYNEARBPGLIGASVGLDIDIRAMRTFVLRYVAODPPFLYFVKVDTGAYDTI 720
Db      661 LFSVLYNEARBPGLIGASVGLDIDIRAMRTFVLRYVAODPPFLYFVKVDTGAYDTI 720
Qy      721 PODRLTEVIASIIKPNVYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLOPYMROFVAHL 780
Db      721 --DLRLTEVIASIIKPNVYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLOPYMROFVAHL 780
Qy      781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRPMCHAVIRKSKVYVQCGIPQGSILSTL 840
Db      781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRPMCHAVIRKSKVYVQCGIPQGSILSTL 840
Qy      841 LSLCIGDMENKLFAGIRRDGLLRVDELLVTHLTHAKTFLTLRVGVEYGVVNL 900
Db      841 LSLCIGDMENKLFAGIRRDGLLRVDELLVTHLTHAKTFLTLRVGVEYGVVNL 900
Qy      901 RKTUVNFPVEDALGETAVVQVPAHGLPWCGLLDTRILEVQSYSSYARSTASTF 960
Db      901 RKTUVNFPVEDALGETAVVQVPAHGLPWCGLLDTRILEVQSYSSYARSTASTF 960
Qy      961 NRGFKAGRMRRRLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYRFLACVLQLP 1020
Db      961 NRGFKAGRMRRRLFGVLRKCHSLFLDQVNSLQTVCTNIYKILLQAYRFLACVLQLP 1020
Qy      1021 FHQGVKNDPFLRIVISTPASLCYSTLKAKNAGMSLGAGAGPJPSEAVQWLCHQATLL 1080
Db      1021 FHQGVKNDPFLRIVISTPASLCYSTLKAKNAGMSLGAGAGPJPSEAVQWLCHQATLL 1080
Qy      1081 KLTRHNVTVPILGSLRTAQTOLSRLLPSTLTALAAANPALPSPDFKTIID 1132
Db      1081 KLTRHNVTVPILGSLRTAQTOLSRLLPSTLTALAAANPALPSPDFKTIID 1132
Qy      1069 KLTRHNVTVPILGSLRTAQTOLSRLLPSTLTALAAANPALPSPDFKTIID 1120

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OS      OS Synthetic.
XX      OS Homo sapiens.
XX      PN GB2317891-A.
XX      PD 08-APR-1998.
XX      PF 01-OCT-1997; 97GB-00020890.
XX      PR 01-OCT-1996; 96US-00724643.
XX      PR 18-APR-1997; 97US-00844419.
XX      PR 25-APR-1997; 97US-00846017.
XX      PR 06-MAY-1997; 97US-00851843.
XX      PR 09-MAY-1997; 97US-00854050.
XX      PR 14-AUG-1997; 97US-00911312.
XX      PR 14-AUG-1997; 97US-00912951.
XX      PR 14-AUG-1997; 97US-00915503.
XX      PA (GERO-) GERON CORP.
XX      PA (UYTE-) UNIV TECHNOLOGY CORP.
XX      PI Cech TR, Langer J, Nakamura T, Chapman KB, Morin GB, Harley CB,
XX      PI Andrews WH;
XX      DR WPI; 1998-171633/16.
XX      PT Pure and recombinant human Telomerase Reverse Transcriptase and its
XX      PT variants - are useful in the diagnosis, prognosis and treatment of cell
XX      PT proliferation conditions especially cancer and ageing.
XX      PS Example 6; Page 231-232; 387pp; English.
XX      CC The present sequence represents a fusion protein from an example of the
XX      CC present invention which describes human telomerase reverse transcriptase
XX      CC (hTERT). The present invention also describes the following methods: (A)
XX      CC determining whether a test compound is a modulator of hTERT, by detecting
XX      CC the change in hTERT recombinant protein or polynucleotide, on
XX      CC administration of the compound; (B) preparation of recombinant telomerase
XX      CC by contacting a protein preparation of hTERT with a telomerase RNA
XX      CC component; (C) detection of the hTERT RNA or protein in a sample by
XX      CC binding a relevant probe to the sample and detecting the complex formed
XX      CC or in the case of RNA detection, amplifying the product and correlating
XX      CC the presence of complex or amplification product with presence of hTERT in
XX      CC the sample; and (D) increasing the proliferation of a vertebrate cell by
XX      CC increasing hTERT expression; and (E) the use of an agent that causes an
XX      CC increase in cell vertebrate cell proliferation to create a medicament
XX      CC that inhibits ageing. A protein preparation of hTERT and the
XX      CC polynucleotide encoding hTERT can be used in the manufacture of
XX      CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
XX      CC telomerase activity can be used to treat conditions that are associated
XX      CC with high telomerase activity. A protein preparation of hTERT can also be
XX      CC used in the new methods
XX      SQ Sequence 1150 AA;
Qy      Query Match 95.8%; Score 5712; DB 2; Length 1150;
Qy      Best Local Similarity 97.6%; Pred. No. 0;
Qy      Matches 110; Conservative 7; Mismatches 6; Indels 14; Gaps 13;
Qy      1 MPRAPRCRAVRSLRSHYREVLPATFVRRLRGQGRVLTORGPAFRALVQCLVCVPM 60
Qy      1 MPRAPRCRAVRSLRSHYREVLPATFVRRLRGQGRVLTORGPAFRALVQCLVCVPM 60
Qy      61 DARPAPAPSFROVSCIKELVAVRLQRLCERGAKNVLAEGFALLDARGGPEAFTTSVR 120
Qy      61 DARPAPAPSFROVSCIKELVAVRLQRLCERGAKNVLAEGFALLDARGGPEAFTTSVR 120
Qy      121 SYLPNTVTDALRSGGAWGLLRVGDVVLHLARCALFVLVAPSCAYOVCGPPLVQLGA 180
Qy      121 SYLPNTVTDALRSGGAWGLLRVGDVVLHLARCALFVLVAPSCAYOVCGPPLVQLGA 180
Qy      121 SYLPNTVTDALRSGGAWGLLRVGDVVLHLARCALFVLVAPSCAYOVCGPPLVQLGA 180
Qy      161 ATQARPAPHASGRRRLICERAMNHSYRAGVPLGAPCARRGGSASRSLLPFRPRR 240

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Db 181 ATGARPPEPHASGPRRLGGERAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRRR 240
 QY 241 GAAPERTPTVGGQSWAHGRTGPRGRCVSVSPAPAEATSLGALGTHSHPSVG 300
 Db 241 GAAPERTPTVGGQSWAHGRTGPRGRCVSVSPAPAEATSLGALGTHSHPSVG 300
 QY 301 ROHHAGPSTSRPRPMDTCPFYATKHFVSSGGKEOLRPSFLSSRLPSTGARRL 360
 Db 301 ROHHAGPSTSRPRPMDTCPFYATKHFVSSGGKEOLRPSFLSSRLPSTGARRL 360
 QY 361 VETIFLGSRPMMGCTPRRLPRLPQRYWQMRPLFELLGNAHGCPRYGLTKHCPLRAVY 420
 Db 361 VETIFLGSRPMMGCTPRRLPRLPQRYWQMRPLFELLGNAHGCPRYGLTKHCPLRAVY 420
 QY 421 PAVGVCAKREKQGVAAPEEEDDPRLVOLLROHSSPMQVGFVAACTRLVPPGL-WG 479
 Db 420 PAVGVCAKREKQGVAAPEEEDDPRLVOLLROHSSPMQVGFVAACTRLVPPGL-WG 479
 QY 480 SRHNERFLLNTKFKFISLGNAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLRE 539
 Db 480 SRHNERFLLNTKFKFISLGNAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLRE 539
 QY 540 ILAKFLHMLMSVYVELLSFFVYTTTFOQNLFFRBSVMSKLSIGRQHLKRYOLR 599
 Db 540 ILAKFLHMLMSVYVELLSFFVYTTTFOQNLFFRBSVMSKLSIGRQHLKRYOLR 599
 QY 599 ELSEAEVROHREARPAITSLRLRFPKPDGLRP-VN-MDYVGARTFRREKRAERLTSTRY 658
 Db 599 ELSEAEVROHREARPAITSLRLRFPKPDGLRP-VN-MDYVGARTFRREKRAERLTSTRY 658
 QY 659 KALFSLVNYRRARRPGLGASVGLDDIHRAKRTFVLRAQDPPELYFVKVDVGAVD 718
 Db 659 KALFSLVNYRRARRPGLGASVGLDDIHRAKRTFVLRAQDPPELYFVKVDVGAVD 718
 QY 719 TIPODRLEVIASLIKQONTVCVRRYAVVOKAAGHRAKFKSHVSTLDLOPYMRQFVA 778
 Db 719 TIPODRLEVIASLIKQONTVCVRRYAVVOKAAGHRAKFKSHVSTLDLOPYMRQFVA 778
 QY 779 HLOETSPLDRAVYVIEOSSSL-NEASSGLPDVFLRFMCNHAIRJGKSYVOCGIPQSGIL 837
 Db 779 HLOETSPLDRAVYVIEOSSSL-NEASSGLPDVFLRFMCNHAIRJGKSYVOCGIPQSGIL 837
 QY 838 STILLCSCYGDMEKRLPAGIRROGLLRLVDDPLVPHLTAKTFLRTIYRQVPEYGV 894
 Db 838 STILLCSCYGDMEKRLPAGIRROGLLRLVDDPLVPHLTAKTFLRTIYRQVPEYGV 894
 QY 898 VNLKRTVNFPEDEALGTAFAVQMPAHGLFPM-CGLLDTRILEVQSDYSYARTSIRA 956
 Db 898 VNLKRTVNFPEDEALGTAFAVQMPAHGLFPM-CGLLDTRILEVQSDYSYARTSIRA 956
 QY 957 SVTPNRCFKAGR-NMRKTLFGLRLKCHSLFLLDQVNSLOTCVTNITYKILLQAVFPAAC 1015
 Db 957 SVTPNRCFKAGR-NMRKTLFGLRLKCHSLFLLDQVNSLOTCVTNITYKILLQAVFPAAC 1015
 QY 1016 VLOLPFQOQWKNPTFLRVIISDTASLCYSILKAKNAGMSLGAKGAGPLPSBAVOMLCH 1075
 Db 1016 VLOLPFQOQWKNPTFLRVIISDTASLCYSILKAKNAGMSLGAKGAGPLPSBAVOMLCH 1075
 QY 1076 QAFLLKLTRHRVTVPLLGSLRTAQOLSRKLPQTTLTALAANPALPSDFKTIID 1132
 Db 1076 QAFLLKLTRHRVTVPLLGSLRTAQOLSRKLPQTTLTALAANPALPSDFKTIID 1132

RESULT 39

AAV00640 ID AAV00640 standard; protein; 1053 AA.

AC AAV00640;

DT 26-JUL-1999 (first entry)

DE Altered C-terminus telomerase protein sequence.

XX

KM Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KM neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KM smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KM stem cell differentiation; organ regeneration; organ differentiation.
 OS Homo sapiens.
 OS Synthetic.
 PN WO9901560-A1.
 PD 14-JAN-1999.
 PF 01-JUL-1998; 98WO-US013835.
 PR 01-JUL-1997; 97US-0051410P.
 PR 21-JUL-1997; 97US-0051018P.
 PR 21-JUL-1997; 97US-0051329P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 PA (CMB-) CAMBIA BIOSYSTEMS LLC.
 PI Kilian A, Bowtell D;
 DR WPI; 1999-106060/09.
 DR N-PSDB; AAX18268.
 PT New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PS growth following injury or bone marrow transplantation.
 PS Claim 4; Fig 111-m; 134pp; English.
 CC This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of hematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilms'
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury. Note: The C-terminus of
 CC this sequence can be replaced by the sequence shown in AAV00654
 XX

Sequence 1053 AA;

Query Match 93.0%; Score 5546; DB 2; Length 1053;

Best Local Similarity 99.8%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 1050; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRRAPRCRAVSSLSLRSHREVPLATFVRRIGPQCMRLVQSGDPAAPAFALVAQCVCVPM 60
 Db 1 MRRAPRCRAVSSLSLRSHREVPLATFVRRIGPQCMRLVQSGDPAAPAFALVAQCVCVPM 60
 QY 61 DARPPAPAPSPROVSCLELVARVLORLCERGANVLAFGFALLDGAAGGPEAFTTSVR 120
 Db 61 DARPPAPAPSPROVSCLELVARVLORLCERGANVLAFGFALLDGAAGGPEAFTTSVR 120
 QY 121 STLPNTVTDALRGSSAKGLLRRVGDVVLVHLARCAFLVVAHSCAYOVGPPYQUGA 180
 Db 121 STLPNTVTDALRGSSAKGLLRRVGDVVLVHLARCAFLVVAHSCAYOVGPPYQUGA 180
 QY 181 ATGARPPEPHASGPRRLGGERAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRRR 240
 Db 181 ATGARPPEPHASGPRRLGGERAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRRR 240
 QY 241 GAAPERTPTVGGQSWAHGRTGPRGRCVSVSPAPAEATSLGALGTHSHPSVG 300

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Db      241 GAPEPERTPVGGSNAHFGTRGSDRGFCVVSAPAEATSLGALSGTRSHSPVG 300
Qy      301 ROHHAGPPTSRPPRWDTPCPVYAETGKFLYSSGDEKQRLPFLSLSLRSLTGARL 360
Db      301 ROHHAGPPTSRPPRWDTPCPVYAETGKFLYSSGDEKQRLPFLSLSLRSLTGARL 360
Qy      361 VETIFLGSPPMGPTRRLPLPQRYWQMRPLFELLGNAACPYGVLKTHCPRAAVT 420
Db      361 VETIFLGSPPMGPTRRLPLPQRYWQMRPLFELLGNAACPYGVLKTHCPRAAVT 420
Qy      421 PAAGVAREKPGGSVAAPBEEDTDRRLVQLRSHSSPMQYGFRACLRRLVPPGLMS 480
Db      421 PAAGVAREKPGGSVAAPBEEDTDRRLVQLRSHSSPMQYGFRACLRRLVPPGLMS 480
Qy      481 RANERFLNTKKFISLGHAKLSLOELTKWMSVEDCAMLRRSPGVCVPAEHLREBEI 540
Db      481 RANERFLNTKKFISLGHAKLSLOELTKWMSVEDCAMLRRSPGVCVPAEHLREBEI 540
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Db      601 LSAEVRQREARPPALTLRLRFIPKPDGLRPIVNMDDYVGARTFRREKRAEHLTSRYKA 660
Qy      661 LRSVLNBERARPPGLIGASVLGDIHRAWRFTVLRPAODPPPLFYKVDTGADYTI 720
Db      661 LRSVLNBERARPPGLIGASVLGDIHRAWRFTVLRPAODPPPLFYKVDTGADYTI 720
Qy      721 POORLEVASIIPKONTVCARVAVVOCAAHGHRKAFKSHSVTLTLOPMROFVAHL 780
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Qy      781 QETSLPDAVVIQSSSLNEASSGLFDVFLRFMCHAVRIRKSYVOCGIPQGSILSTL 840
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Qy      841 LSLCYGDMENKLPAGIRRDGLLRVNDPLVTLPHLTHAKELTLTRGVPEVCVNL 900
Db      841 LSLCYGDMENKLPAGIRRDGLLRVNDPLVTLPHLTHAKELTLTRGVPEVCVNL 900
Qy      901 RKTVPNFPVEDEALGTAFCVMPAHGLFPWGLLIDTRTLEVOSSYASRTSIRASYTF 960
Db      901 RKTVPNFPVEDEALGTAFCVMPAHGLFPWGLLIDTRTLEVOSSYASRTSIRASYTF 960
Qy      961 NRGFKAGRNRRKLFGVLRKCHSLFLDQVNSLQTVCTNIXKILLQAYRHHACVQLP 1020
Db      961 NRGFKAGRNRRKLFGVLRKCHSLFLDQVNSLQTVCTNIXKILLQAYRHHACVQLP 1020
Qy      1021 FHQGVKNPFFLRVISTPASLCYSILKAKNA 1052
Db      1021 FHQGVKNPFFLRVISTPASLCYSILKAKNA 1052

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RESULT 40

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AA00649
ID AA00649 standard; protein; 1093 AA.
XX
AC AA00649;
XX
DT 26-JUL-1999 (first entry)
XX
DE Altered C-terminus telomerase (ver. 2) protein sequence.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
XX
SY Synthetic.
XX

```

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PN      W09901560-A1.
XX      14-JAN-1999.
XX      01-JUL-1998; 98MO-US013835.
XX      01-JUL-1997; 97US-0051410P.
XX      21-JUL-1997; 97US-0053018P.
XX      21-JUL-1997; 97US-005329P.
XX      04-AUG-1997; 97US-0054642P.
XX      09-SEP-1997; 97US-0058287P.
XX      (CMB-) CAMBIA BIOSYSTEMS LLC.
XX      Killian A, Bowtell D;
XX      WPI; 1999-106060/09.
XX      DR N-PSDB; AAX18277.
XX      PT New isolated vertebrate telomerase genes - used to develop products for
XX      treating cancers or for organ regeneration, nerve cell or brain cell
XX      growth following injury or bone marrow transplantation.
XX      Claim 4; Fig 11af-ag; 134p; English.
XX
CC      This sequence is a truncated human telomerase of the invention. Primers
CC      that amplify the telomerase coding sequence can be used in a method for
CC      diagnosing cancer in a patient. The telomerase can be used for detection,
CC      diagnosis and drug screening. Inhibitors of telomerase activity can be
CC      used to treat cancers such as melanomas, other skin cancers,
CC      neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
CC      lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC      growths. Enhancers of telomerase may be used to stimulate stem cell
CC      proliferation and differentiation (expansion of haematopoietic stem cells
CC      could be administered in the bone marrow transplant context). As well,
CC      many tissues have stem cells. Proliferation of these cells may be useful
CC      in wound healing, hair growth, treatment of disease such as Wilm's
CC      tumour, organ regeneration or differentiation after injury or diseases,
CC      nerve cell or brain cell growth following injury. Note: The N-terminus of
CC      this sequence can be replaced by the sequences shown in AA00656-Y00658,
CC      and the C-terminus can be replaced by the sequence shown in AA00654
XX
SQ      Sequence 1093 AA;
XX
Query Match 92.4%; Score 5507; DB 2; Length 1093;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 1045; Conservative 1; Mismatches 2; Indels 40; Gaps 1;

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Db 361 VETIFGSRPMMPTGPRRLPRLPQRYWQRPFLLELLGNHACPYGLLKHCPRLAAVT 420
QY 421 PAAGVCAREKPPQGSVAAPPEEDDPRLVOLLRQSSPMQVGFVACLRILVPRGLMGS 480
Db 421 PAAGVCAREKPPQGSVAAPPEEDDPRLVOLLRQSSPMQVGFVACLRILVPRGLMGS 480
QY 481 RHNERREPLRNTKKFISLGHAKLSLOE----- 507
Db 481 RHNERREPLRNTKKFISLGHAKLSLOELTWKMSVRCAMLRSPGVGCPAAEHLREBI 540
QY 508 -----LTKMSVRCAMLRSPGVGCPAAEHLREBI 560
Db 541 LAKFLHMLTWKMSVRCAMLRSPGVGCPAAEHLREBI 600
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Db 601 FYVTETTFQKNRLFEYRPSVMSKLOSIGIRQHLKRVOLRELSAEVROHREARPALITSR 660
QY 621 LRPIPKPDGLRPIVNDYVVGARTFRERKRAERLTSRKALFSVLNERARPRGLGASY 680
Db 661 LRPIPKPDGLRPIVNDYVVGARTFRERKRAERLTSRKALFSVLNERARPRGLGASY 720
QY 681 LGJDDIHRARMTFLVRAQDPPELYFVKVDVTGAYDTIPQDLTEVLASIIKQNTYC 740
Db 721 LGJDDIHRARMTFLVRAQDPPELYFVKVDVTGAYDTIPQDLTEVLASIIKQNTYC 780
QY 741 VRXYAVVQKAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLDAVIEQSSLINE 800
Db 781 VRXYAVVQKAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLDAVIEQSSLINE 840
QY 801 ASSGLFPVFLRPMCHAVRIRGKS YVOCQGIPOGSIISTLLCGLCYGDMENKLPAGIRRD 860
Db 841 ASSGLFPVFLRPMCHAVRIRGKS YVOCQGIPOGSIISTLLCGLCYGDMENKLPAGIRRD 900
QY 861 GLILRLVDDFLVTPHLTHAKTFLRTVIRGVPEXGCYVNLRTVNFVPEDEALGTAFFV 920
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QY 981 KCHSLFELDLQVNSIQVCTNIYKILILQAYRFAVCYLQLPFHQVWKNPFFELRVISDTA 1040
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QY 1041 SLCYSIUKAKNA 1052
Db 1081 SLCYSIUKAKNA 1092

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Job time : 112 secs

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Tue Dec 21 15:43:30 2004

us-08-974-584c-118.ra1

Page 1

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OM protein - protein search, using sw model

Run on: December 20, 2004, 15:55:46 ; Search time 42 Seconds
(without alignments)
1787.428 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6638000 residues
Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 120 summaries

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6: /cgn2_6/prodata/1/iaa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5963	100.0	1132	3	US-08-974-549A-344 Sequence 344, App
2	5963	100.0	1132	4	US-09-402-181B-344 Sequence 344, App
3	5963	100.0	1132	4	US-09-721-456B-344 Sequence 344, App
4	5963	100.0	1407	3	US-08-974-549A-628 Sequence 628, App
5	5963	100.0	1407	4	US-08-912-951-334 Sequence 334, App
6	5963	100.0	1407	4	US-09-402-181B-628 Sequence 628, App
7	5963	100.0	1407	4	US-09-721-456B-628 Sequence 628, App
8	5952	99.8	1132	3	US-08-851-843A-225 Sequence 225, App
9	5952	99.8	1132	3	US-08-974-549A-225 Sequence 225, App
10	5952	99.8	1132	3	US-08-854-050-225 Sequence 225, App
11	5952	99.8	1132	3	US-09-430-323-225 Sequence 225, App
12	5952	99.8	1132	3	US-09-128-354-225 Sequence 225, App
13	5952	99.8	1132	4	US-09-675-321-225 Sequence 225, App
14	5952	99.8	1132	4	US-09-052-919-225 Sequence 225, App
15	5952	99.8	1132	4	US-08-912-951-225 Sequence 225, App
16	5952	99.8	1132	4	US-09-402-181B-225 Sequence 225, App
17	5952	99.8	1132	4	US-09-721-456B-225 Sequence 225, App
18	5952	99.8	1132	4	US-09-953-052-225 Sequence 225, App
19	5952	99.8	1132	4	US-09-042-460-323 Sequence 323, App
20	5952	99.8	1132	3	US-08-974-549A-611 Sequence 611, App
21	5952	99.8	1154	4	US-08-912-951-323 Sequence 323, App
22	5952	99.8	1154	4	US-09-402-181B-611 Sequence 611, App
23	5952	99.8	1154	4	US-09-721-456B-611 Sequence 611, App
24	5952	99.8	1189	3	US-08-974-549A-613 Sequence 613, App
25	5952	99.8	1189	4	US-08-912-951-325 Sequence 325, App
26	5952	99.8	1189	4	US-08-402-181B-613 Sequence 613, App
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28	5952	99.8	1200	3	US-08-974-549A-612 Sequence 612, App
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30	5952	99.8	1200	4	US-09-402-181B-612 Sequence 612, App
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33	5952	99.8	1285	4	US-08-912-951-114 Sequence 314, App
34	5952	99.8	1285	4	US-08-912-951-114 Sequence 314, App
35	5952	99.8	1285	4	US-09-402-181B-600 Sequence 600, App
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41	3810.5	63.9	1003	3	US-08-974-549A-336 Sequence 336, App
42	3810.5	63.9	1003	3	US-08-854-050-217 Sequence 217, App
43	3810.5	63.9	1003	3	US-09-430-323-217 Sequence 217, App
44	3810.5	63.9	1003	4	US-09-402-181B-336 Sequence 336, App
45	3810.5	63.9	1003	4	US-09-721-456B-336 Sequence 336, App
46	3496	58.6	1122	4	US-09-042-460-225 Sequence 225, App
47	3125	52.4	622	4	US-09-582-924B-112 Sequence 112, App
48	2178	36.5	438	4	US-09-582-924B-112 Sequence 112, App
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50	2079	34.9	564	3	US-08-851-843A-101 Sequence 101, App
51	2079	34.9	564	3	US-08-974-549A-267 Sequence 267, App
52	2079	34.9	564	3	US-08-854-050-101 Sequence 101, App
53	2079	34.9	564	3	US-09-430-323-101 Sequence 101, App
54	2079	34.9	564	3	US-09-402-181B-267 Sequence 267, App
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56	1666.5	27.9	538	3	US-08-974-549A-602 Sequence 602, App
57	1666.5	26.2	538	4	US-08-912-951-316 Sequence 316, App
58	1666.5	26.2	538	4	US-08-912-951-320 Sequence 320, App
59	1666.5	26.2	538	4	US-09-402-181B-606 Sequence 606, App
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71	1447	24.3	530	4	US-09-402-181B-603 Sequence 603, App
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73	1438	24.1	583	4	US-09-424-226-604 Sequence 604, App
74	1386	23.2	515	3	US-08-974-549A-604 Sequence 604, App
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78	1243.5	20.9	364	4	US-09-417-485D-41 Sequence 41, App
79	1090	18.3	259	3	US-08-974-549A-100 Sequence 100, App
80	1090	18.3	259	4	US-08-912-951-110 Sequence 110, App
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82	1090	18.3	259	4	US-09-721-456B-110 Sequence 110, App
83	929	15.6	222	3	US-08-851-843A-202 Sequence 202, App
84	929	15.6	222	3	US-08-974-549A-321 Sequence 321, App
85	929	15.6	222	3	US-08-854-050-203 Sequence 203, App
86	929	15.6	222	3	US-08-854-050-203 Sequence 203, App
87	929	15.6	222	3	US-09-430-323-202 Sequence 202, App
88	929	15.6	222	4	US-09-402-181B-321 Sequence 321, App
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97	646	10.8	129	3	US-08-851-843A-67 Sequence 67, App
98	646	10.8	129	3	US-08-974-549A-13 Sequence 13, App
99	646	10.8	129	3	US-08-854-050-67 Sequence 67, App
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 113 440.5 7.4 1007 3 US-08-851-843A-86
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ALIGNMENTS

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 Sequence 69, App1
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 Sequence 189, App1
 Sequence 86, App1
 Sequence 86, App1
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 Sequence 187, App1
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 Sequence 2, App1
 Sequence 110, App1

RESULT 1
 US-08-974-549A-344
 ; Sequence 344, Application US/08974549A
 ; Patent No. 6166178
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Hartley, Calvin B.
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Human telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 727
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,549A
 ; FILING DATE: 19-NOV-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/854,050
 ; FILING DATE: 09-MAY-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/911,312
 ; FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 344:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-974-549A-344

Query Match 100.0%; Score 5963; DB 3; Length 1132;
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 DB 601 LSAEVRQREARPALITRLRFIRKPDGLRIVMDVYVGARTRRERARLRSRYA 660

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Db 601 LSEAEVROHREARPAALLTSRLRPIPKPDGLRPIVNDYVVGARTFRREKRAEELTSRYKA 660
Qy 661 LFSVLNVERARRRGLGASVYLGDDJHRAWRTVLEVRARODPEPELYFVKVDTAGYDTI 720
Db 661 LFSVLNTERARRRGLGASVYLGDDJHRAWRTVLEVRARODPEPELYFVKVDTAGYDTI 720
Qy 721 PQRLTEVIAIITKPPONTYCVRRYAVVQKAHSHVKAFAKSHVSTLTLDQPYMRQFVAHL 780
Db 721 PQRLTEVIAIITKPPONTYCVRRYAVVQKAHSHVKAFAKSHVSTLTLDQPYMRQFVAHL 780
Qy 781 QETSPLADAVIIOSSSLNASSGGLFVFLRFMCHHVAIRRGSYVQCGIPQGSILSTL 840
Db 781 QETSPLADAVIIOSSSLNASSGGLFVFLRFMCHHVAIRRGSYVQCGIPQGSILSTL 840
Qy 841 LGSLLCYGDMENKLFAGIRDDGLLRVDLVTPLHTRAKTFLRLVGVPEYGCVANL 900
Db 841 LGSLLCYGDMENKLFAGIRDDGLLRVDLVTPLHTRAKTFLRLVGVPEYGCVANL 900
Qy 901 RKTVAAPFVDEALGTAFAVQMPAHGLFPWCGLLDLTRILEVQSDYSYARISIRASVTF 960
Db 901 RKTVAAPFVDEALGTAFAVQMPAHGLFPWCGLLDLTRILEVQSDYSYARISIRASVTF 960
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Db 961 NRGFKAGRMNRKLFVGLRLKCHSLFLDLQVNSLQVCTNIYKILLQAVRFHACVLOLP 1020
Qy 1021 FHQVKNKPFELRLVISTDASLCYSILKANAGMSLGAKGAPLPSEAVOMLCHOAFIL 1080
Db 1021 FHQVKNKPFELRLVISTDASLCYSILKANAGMSLGAKGAPLPSEAVOMLCHOAFIL 1080
Qy 1081 KLTRHRRTYVPLGLSLRTAQTOLSRKLPJTTLTALBAANPALPSPFKTIL 1132
Db 1081 KLTRHRRTYVPLGLSLRTAQTOLSRKLPJTTLTALBAANPALPSPFKTIL 1132

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RESULT 2

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US-09-402-181B-344
; Sequence 344, Application US/09402181B
; Patent No. 6610839

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GENERAL INFORMATION:

```

APPLICANT: Cech, Thomas R.

```

```

Inventor: Joachim

```

```

Nakamura, Toru

```

```

Morth, Gregg B.

```

```

Harley, Calvin B.

```

```

Andrews, William H.

```

```

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

```

```

NUMBER OF SEQUENCES: 633

```

```

CORRESPONDENCE ADDRESS:

```

```

ADDRESS: Townsend and Townsend and Crew LLP

```

```

STREET: Two Embarcadero Center, Eighth Floor

```

```

CITY: San Francisco

```

```

STATE: California

```

```

COUNTRY: USA

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ZIP: 94111-3834

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COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk

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OPERATING SYSTEM: IBM PC compatible

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SOFTWARE: Patentin Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/402,181B

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FILING DATE: 29-Sep-1997

```

```

CLASSIFICATION: <unknown>

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PRIORITY APPLICATION DATA:

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APPLICATION NUMBER: US 08/724,643

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FILING DATE: 01-OCT-1996

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```

APPLICATION NUMBER: US 08/844,419

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FILING DATE: 18-APR-1997

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APPLICATION NUMBER: US 08/846,017

```

```

FILING DATE: 25-APR-1997

```

```

APPLICATION NUMBER: US 08/851,843

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; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Auenhue, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 344:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 344:
US-09-402-181B-344

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Query Match 100.0%; Score 5963; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 DARPPAAPSFRQVSCLELVAARVQLRCERGANVLAFGALLDGAAGPPEAFTTSVR 120
Qy 121 SYLPTVTDALRGSAWLLLRVQDDVYHLRLCALFVLVAPSCAQQVGGPPLVYQGA 180
Db 121 SYLPTVTDALRGSAWLLLRVQDDVYHLRLCALFVLVAPSCAQQVGGPPLVYQGA 180
Qy 181 ATQARPPHAAGPRRLRCERAMNHSVEAGVPLGLPAPGARRGGSASRLPLPKRPRR 240
Db 181 ATQARPPHAAGPRRLRCERAMNHSVEAGVPLGLPAPGARRGGSASRLPLPKRPRR 240
Qy 241 GAAPPERTPVQGGWAMHPRGTGSGDRGFCVSPAPAEATSLSEGLSGTRISHPEVG 300
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Db 361 VETIFLGRPMWPGTFRRLPRLPORVWQMRPLFELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAEKEQGSVAAREEDTPRRVYOLLRHSSWQVYGFARCLARLVPGWLGS 480
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Qy 481 RHNERRFLRNTKFFSLGKHAKLSLOELTWKSYVDCAMLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERRFLRNTKFFSLGKHAKLSLOELTWKSYVDCAMLRSPGVGCVPAAEHRLREI 540
Qy 541 LAKFLHMLMSYVVELLASFVYVETTFQKRLFFYRSVSKLSIGIRQLKRVQURE 600
Db 541 LAKFLHMLMSYVVELLASFVYVETTFQKRLFFYRSVSKLSIGIRQLKRVQURE 600
Qy 601 LSEAEVROHREARPAALLTSRLRPIPKPDGLRPIVNDYVVGARTFRREKRAEELTSRYKA 660

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DB 601 LSEAEVQRHREARPAALLTSRLAFIRKPGDLRIYVMYDVVGARTERREKRAERTLSRYKA 660
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DB 661 LFSVLYNEARRRPGLIGASVGLGDDIHRAMRTFVLVRADDPPELVYVVKVDVYGAYYTI 720
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DB 721 PODRLTEVIASITIKPONTYCVARVAVVOGAHGHVRAKFKSHVSTLTDLQPYMROFVAHL 780
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DB 781 QETSPIRDAVVIQOSSLINEASSGLFDVFLRMCHAVIRKGSVVOCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLPAGIRRDGLLRLVDDFLVTEHLTHAKTFLTLVGVPEYGVVNL 900
DB 841 LCSLCYGMENKLPAGIRRDGLLRLVDDFLVTEHLTHAKTFLTLVGVPEYGVVNL 900
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DB 901 RTVVNFPEDBALGOTAVOMPAHGLPWCGLLDTRTLEVQSGSYASTSTRASTF 960
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DB 1021 FHQOVKMPFFLRYISDTASLCYSILKAKAKGSLGAKGAGPLPSAVOMLCHQATLL 1080
QY 1081 KLTRHRTVYVPLGSLRTAQOTLSRKLPGTTLTLEAANPALPDPDFITLD 1132
DB 1081 KLTRHRTVYVPLGSLRTAQOTLSRKLPGTTLTLEAANPALPDPDFITLD 1132

RESULT 3
US-09-721-456-344
Sequence 344, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 344:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 344:
US-09-721-456-344
Query Match 100.0%; Score 5963; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLIRSHYREVLPLATFVRRLCPQGRVLVQSGDPAAFRALVAQCLVCVW 60
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DB 421 PAAGVCAAREKPOGSVAAPBEEDTDPRLVQLLRQSSPQVGYFVACLRILVPGLMGS 480
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 Db 721 PQRLEFVIAIIRKPTNTYCVRRYAVOKAHGVRKAFKSHVSTLTDLQPYWRQFVAHI 780
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 QY 961 NRGFKAQRNMRRLFGVLRKCHSLFLDLQVNSLQTVCTNYKILLQAYRPAVCYLOLP 1020
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 Db 1021 FHOQVKNPFFPRVTSIDTASLCYSILKAKNAQMSIGAKAAGPPLSEAVQWICHOAFL 1080
 QY 1081 KLTRHRTVYPLIGSLRTAQTOLSRKLPFTTLTALBAANPALPSFKTILD 1132
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QY 1 MPRAPRCAGVSLIRSHRYEVLPLATFVRRLPGQGWELVQGRDPAARALVAOCLVCVPM 60
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 QY 61 DARPPAPSPFROYSCUXELVAVYLOSLCERGANVLAFGFALDDGARGGPPPAFTTSVR 120
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 QY 121 SYLPTVTDALRGSGANGLLIRVGDVYVHLLARCALFVYVAVSCAYVCGPPLYLQGA 180
 Db 396 SYLPTVTDALRGSGANGLLIRVGDVYVHLLARCALFVYVAVSCAYVCGPPLYLQGA 455
 QY 181 ATQARPPPHASGPRRRIGCERAMNHSVREAGVPLGLPAPGARRRGSGASSLPLPKRPRR 240
 Db 456 ATQARPPPHASGPRRRIGCERAMNHSVREAGVPLGLPAPGARRRGSGASSLPLPKRPRR 515
 QY 241 GAAPPERTPVGQSSNAHPGRTGSPDRGFCVVSPPAPAEATSLSEALGSTRSHSVG 300
 Db 516 GAAPPERTPVGQSSNAHPGRTGSPDRGFCVVSPPAPAEATSLSEALGSTRSHSVG 575

Query Match 100.0%; Score 5963; DB 3; Length 1407;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-974-549A-628
 RESULT 4
 US-08-974-549A-628
 ; Sequence 628, Application US/08974549A
 ; Patent No. 6166178
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin B.
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 727
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,549A
 ; FILING DATE: 19-NOV-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 628:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1407 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1407
 OTHER INFORMATION: /note= "fusion protein composed of
 OTHER INFORMATION: enhanced green fluorescent protein
 OTHER INFORMATION:
 OTHER INFORMATION: 5' untranslated region of hTERT mRNA and
 hTERT protein sequence"

QY 301 ROHAGPSTSRPPWPMDTCCPPVYAEKHFLLYSAGDKEDLPSEFLLSLRPSLTGARRL 360
 DB 576 ROHAGPSTSRPPWPMDTCCPPVYAEKHFLLYSAGDKEDLPSEFLLSLRPSLTGARRL 635
 QY 361 VETIFLGSRRPWPMDTCCPPVYAEKHFLLYSAGDKEDLPSEFLLSLRPSLTGARRL 420
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 QY 421 PAAGCAEKEKPGQSVAAPEEEDTDRRLVOLLROHSSPMQYGVRACTRLVPPGIMGS 480
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 QY 481 RANERFLRNTKFFISLGHAKLSIOELTWKMSVDCAMLRSPQGVCPAAERLRBEI 540
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 DB 1056 QETSPLRDAVLEIOSSSINEASSGLFDVLEFMECHAVRIRGKSYVQCGIPQSSILSTL 1115
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 DB 1236 NRGFKAGNMRRKLFQVLRKCHSLFDLQVNSLQVCTNLYKILLQAYRHHACVQLP 1295
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 DB 1356 KLTRHRVTVPLGLSLRTAQOLSRKLPCTTLTALAAANPALPBDFTIIL 1407
 RESULT 5
 US-08-912-951-334
 Sequence 334, Application US/08912951
 Patent No. 6475789
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 THERAPEUTIC METHODS
 NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 City: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/912,951
 FILING DATE: 14-AUG-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 03-MAY-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 334:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1407 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-912-951-334
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 Best Local Similarity 100.0%; Pred. No. 0;
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Db 696 PAAGVCAKREKQSVAPAEEDDPRLVQLAQSHPWQVGFVRAACLRVLPRLKMS 755
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RESULT 6

US-09-402-181B-628

Sequence 628, Application US/09402181B

Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

Inventor: Joachim

Nakamura, Toru

Chapman, Karen B.

Morth, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

```

NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aussenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 628:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1407
OTHER INFORMATION: /note= "fusion protein composed of
enhanced green fluorescent protein
(EGFP) residues, residues encoded by the
5' untranslated region of hTERT mRNA and
hTERT protein sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 628:
US-09-402-181B-628

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Query Match 100.0%; Score 5963; DB 4; Length 1407;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
 US-09-721-456-628
 ; Sequence 628, Application US/09721456
 ; Patent No. 6617110

GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Hartley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESS: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
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 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,456
 FILING DATE: 22-Nov-6617110-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17685
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 628:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1407 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1407
 OTHER INFORMATION: /note="fusion protein composed of
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 5' untranslated region of hTERT mRNA and
 hTERT protein sequence"
 SEQUENCE DESCRIPTION: SEQ ID NO: 628:
 US-09-721-456-628

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 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8

US-08-851-843A-225
 Sequence 225, Application US/08851843A
 Patent No. 6093809

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.
 APPLICANT: Ingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: No. 6093809e1 Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESS: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/851.843A
 FILING DATE: 06-MAY-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 225:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid

TOPOLOGY:

TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-851-843A-225

Query Match 99.8%; Score 5952; DB 3; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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661 LPSVLYNEARPPGLIGASVGLDIDIRAMRTFVLRVAODPPPLVYKVDVGAVTI 720
721 PODRLTEVASTIKPONTVCARVAVOQKAHGRKAFKSHVSTLTLOPYMQFVAHL 780
721 PODRLTEVASTIKPONTVCARVAVOQKAHGRKAFKSHVSTLTLOPYMQFVAHL 780
781 QETSPJRDAVIEOSSSINEASSGLFDFVLRPMCHAVIRKSYVQCGIPQGSILSTL 840
781 QETSPJRDAVIEOSSSINEASSGLFDFVLRPMCHAVIRKSYVQCGIPQGSILSTL 840
841 LGSICGDMENKLPAGIRRDGLLRLVDPFLVTPHLLTHAKFTLTVRGVPEGCYVNL 900
841 LGSICGDMENKLPAGIRRDGLLRLVDPFLVTPHLLTHAKFTLTVRGVPEGCYVNL 900
901 RKTIVNFPVEDALGGTAFCVMPAHGLFPWCGLLLDTRTLEVOSSYVARTSIRAVTF 960
901 RKTIVNFPVEDALGGTAFCVMPAHGLFPWCGLLLDTRTLEVOSSYVARTSIRAVTF 960
961 NGGFKAGRMERKLEVLKCHSLFLDQVNSLQTVCNITKILLQAYFHAQVOLDP 1020
961 NGGFKAGRMERKLEVLKCHSLFLDQVNSLQTVCNITKILLQAYFHAQVOLDP 1020
1021 FHQQVKNFTFLRVIDSTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOWLCHQATLL 1080
1021 FHQQVKNFTFLRVIDSTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOWLCHQATLL 1080
1081 KLTRRVTYVPLGLSRTAQTOLSRKLPSTTTTALBAANPALBEDFTIILD 1132
1081 KLTRRVTYVPLGLSRTAQTOLSRKLPSTTTTALBAANPALBEDFTIILD 1132

RESULT 9
US-08-974-549A-2
Sequence 2, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear

Tue Dec 21 15:43:30 2004

us-08-974-584c-118.ra1

Page 11

MOLECULE TYPE: protein
US-08-974-549A-2

Query Match 99.8%; Score 5952; DB 3; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAFCRAVRSILRSHREVLPATFVRSLGQGMELVORGDPAAFRALVAQCLVCPM 60
DB 1 MPRAFCRAVRSILRSHREVLPATFVRSLGQGMELVORGDPAAFRALVAQCLVCPM 60
QY 61 DARPPAPASFRQVSCIKELVAVLQRLCERGAKNVLAFFALLDARGPPEAFTTSR 120
DB 61 DARPPAPASFRQVSCIKELVAVLQRLCERGAKNVLAFFALLDARGPPEAFTTSR 120
QY 121 SYLPNTVTDALRGSGAGMLLRVGGDVLVHLARCAFLVAPSCAYQYCGPPLVQLGA 180
DB 121 SYLPNTVTDALRGSGAGMLLRVGGDVLVHLARCAFLVAPSCAYQYCGPPLVQLGA 180
QY 181 ATQARPPHAGSGPRRLGCEBAMNHSYREXGVPGLPAPCARRGSGASLSLPRKPR 240
DB 181 ATQARPPHAGSGPRRLGCEBAMNHSYREXGVPGLPAPCARRGSGASLSLPRKPR 240
QY 241 GAAPERTPTVQGSNMHPGTRGSDRGFCVSPAPAEATSLGALSCTHSHPSVQ 300
DB 241 GAAPERTPTVQGSNMHPGTRGSDRGFCVSPAPAEATSLGALSCTHSHPSVQ 300
QY 301 ROHHAGPSTSRPPMDTCPVYATKHFVSSGDEQLRPSFLISSLRPSLTGAARL 360
DB 301 ROHHAGPSTSRPPMDTCPVYATKHFVSSGDEQLRPSFLISSLRPSLTGAARL 360
QY 361 VETTFGSRPMGCTPRRLPRLPORVQWRPLFELIGNACCPYGLKTHQCLTAAYT 420
DB 361 VETTFGSRPMGCTPRRLPRLPORVQWRPLFELIGNACCPYGLKTHQCLTAAYT 420
QY 421 PAACVCAKREKQGSVAAPBEEDTDPRRLVOLLROHSSPMOYVGFVAQLRLVPGIWS 480
DB 421 PAACVCAKREKQGSVAAPBEEDTDPRRLVOLLROHSSPMOYVGFVAQLRLVPGIWS 480
QY 481 RHNERRRLRNTKRTISLGAKAKLSLOELTWKMSYRDCAMLRSGVCAVAHRREEL 540
DB 481 RHNERRRLRNTKRTISLGAKAKLSLOELTWKMSYRDCAMLRSGVCAVAHRREEL 540
QY 541 LAKELHMLSVYVELRSEFFVETTFQKNRLFFPYRPSWSKLSIGIQHLKRYOLRE 600
DB 541 LAKELHMLSVYVELRSEFFVETTFQKNRLFFPYRPSWSKLSIGIQHLKRYOLRE 600
QY 601 LSEAVERQHRERAPALLTSRLRFPKPDGLRPIVMDYVVGARTFRERKAERLTSRVA 660
DB 601 LSEAVERQHRERAPALLTSRLRFPKPDGLRPIVMDYVVGARTFRERKAERLTSRVA 660
QY 661 LFSVLANERARRPGLLGSVGLDDIHRAMTFVLRAADPPBELFVAVDTGAVDTI 720
DB 661 LFSVLANERARRPGLLGSVGLDDIHRAMTFVLRAADPPBELFVAVDTGAVDTI 720
QY 721 PODRLTEVIAASIKPQNTYCVRRYAVVQKAHGHVRAKFSHVSTLTDLPYRQFVAHL 780
DB 721 PODRLTEVIAASIKPQNTYCVRRYAVVQKAHGHVRAKFSHVSTLTDLPYRQFVAHL 780
QY 781 QETSEPLDVAVITESSSINASSGLFDVPLRFPMCHAVRIRGKSYYOCCOIIPOGSIISTL 840
DB 781 QETSEPLDVAVITESSSINASSGLFDVPLRFPMCHAVRIRGKSYYOCCOIIPOGSIISTL 840
QY 841 LCSLCYGDMEKTLFAGIRRDGILLRLVDDFLVTPHLTHAKFTLTLVRGPEYGVNL 900
DB 841 LCSLCYGDMEKTLFAGIRRDGILLRLVDDFLVTPHLTHAKFTLTLVRGPEYGVNL 900
QY 901 RKTIVNPFVDEALGGTAFVQMPAHGLFPMCGLLIDRLTEVOSDYSSYARTSIRASLTF 960
DB 901 RKTIVNPFVDEALGGTAFVQMPAHGLFPMCGLLIDRLTEVOSDYSSYARTSIRASLTF 960
QY 961 NRGFAGNRMRKLFGLVRLKCHSLFLDLQVNSLQTCNTNYKILLQAFRHACVQLP 1020

DB 961 NRGFAGNRMRKLFGLVRLKCHSLFLDLQVNSLQTCNTNYKILLQAFRHACVQLP 1020
QY 1021 FHQVWKNPTEFLRYISDTASLCYSILKAKNAGMSLGAKGAGPLPSBAVOMLCHQAFLL 1080
DB 1021 FHQVWKNPTEFLRYISDTASLCYSILKAKNAGMSLGAKGAGPLPSBAVOMLCHQAFLL 1080
QY 1081 KLTRHRVTVVPLGSLRFAQTOLSRKLPGLTTLTALEAANPALPSDFXTILD 1132
DB 1081 KLTRHRVTVVPLGSLRFAQTOLSRKLPGLTTLTALEAANPALPSDFXTILD 1132

RESULT 10
US-08-854-050-225

Sequence 225, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Czech, Thomas R.
APPLICANT: Langner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997

CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-854-050-225

Query Match 99.8%; Score 5952; DB 3; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILSRHYREVLPLATFVRRLGQGNVLVQGDPAFRLVAQCLVCVPM 60
Db 1 MPAPRCRAVRSILSRHYREVLPLATFVRRLGQGNVLVQGDPAFRLVAQCLVCVPM 60

QY 61 DAPPPAASFRVSCLEKELVARVLOQLCEGAKVLAFGPALLGARGPPEAFTTSVR 120
Db 61 DAPPPAASFRVSCLEKELVARVLOQLCEGAKVLAFGPALLGARGPPEAFTTSVR 120

QY 121 SYLPNTVTDALRSGAGMGLLRVRGDDVLWHLLARCALFVLAFCAYQVCGPRLYOLGA 180
Db 121 SYLPNTVTDALRSGAGMGLLRVRGDDVLWHLLARCALFVLAFCAYQVCGPRLYOLGA 180

QY 181 ATGAPRPPHAGSGRRRLGGERAMNHSVRAGVPLGIPAGARRRGSASRSPLKRRR 240
Db 181 ATGAPRPPHAGSGRRRLGGERAMNHSVRAGVPLGIPAGARRRGSASRSPLKRRR 240

QY 241 GAAPERTPVGGGSAHGGRTGSPDRGFCVSPAPAEATSLGALSGTRHSPSVG 300
Db 241 GAAPERTPVGGGSAHGGRTGSPDRGFCVSPAPAEATSLGALSGTRHSPSVG 300

QY 301 RQHHAGPSTSRPPRWDTPCPPVYAEKHFYSSGDKQLRPSLSSLRSLTGARRL 360
Db 301 RQHHAGPSTSRPPRWDTPCPPVYAEKHFYSSGDKQLRPSLSSLRSLTGARRL 360

QY 361 VETIFGSRPMWGTERRPLPLPORYOKRPLFLELGNHACPYGLTKHCPLRAVT 420
Db 361 VETIFGSRPMWGTERRPLPLPORYOKRPLFLELGNHACPYGLTKHCPLRAVT 420

QY 421 PAAGVCAKREKPOGSVAPEEDTDPRLVOLLRQHSSPMOYGVFYACLRRLVPGMGS 480
Db 421 PAAGVCAKREKPOGSVAPEEDTDPRLVOLLRQHSSPMOYGVFYACLRRLVPGMGS 480

QY 481 RHNERPFLNTKFFSLGKHAFLSLOELTWKMSVDCALRRSPGVGCPAAEHRLREI 540
Db 481 RHNERPFLNTKFFSLGKHAFLSLOELTWKMSVDCALRRSPGVGCPAAEHRLREI 540

QY 541 LAKFLHMLSVYVVELLRSEFFVTEFTFOKNRLFYRPSVMSKLOSIGIRHLKEVORE 600
Db 541 LAKFLHMLSVYVVELLRSEFFVTEFTFOKNRLFYRPSVMSKLOSIGIRHLKEVORE 600

QY 601 LBSAEVRORREARPALITSLRFLIPKPOLRPIVNMDDYVAGARTRRERARLRSYKA 660
Db 601 LBSAEVRORREARPALITSLRFLIPKPOLRPIVNMDDYVAGARTRRERARLRSYKA 660

QY 661 LBSVLYERARRPGLIGASVGLGDIDIRAMRTFVLVRADPPPELYFKVDVTGADTI 720
Db 661 LBSVLYERARRPGLIGASVGLGDIDIRAMRTFVLVRADPPPELYFKVDVTGADTI 720

QY 721 PODRLTEVIASIIKPNNTYCVRRYAVVQKAHGHVKAFFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNNTYCVRRYAVVQKAHGHVKAFFKSHVSTLTDLOPYMRQFVAHL 780

QY 781 QETSPFRDAVVIQOSSSLNEASSGLFDVLFMCHHAARIRKGSVVOCGIPQSSILSTL 840
Db 781 QETSPFRDAVVIQOSSSLNEASSGLFDVLFMCHHAARIRKGSVVOCGIPQSSILSTL 840

QY 841 LCSLCYGDMMENKLPAGIRRDGLLRIVDDFLLVTDHLLTHAKTFLRTLVAGVEYCVNVL 900
Db 841 LCSLCYGDMMENKLPAGIRRDGLLRIVDDFLLVTDHLLTHAKTFLRTLVAGVEYCVNVL 900

QY 901 RKTUVNFPVEDALGTAFCVMPAHGIPWCGILLDTFTLIVQSSYASRTSRASTF 960
Db 901 RKTUVNFPVEDALGTAFCVMPAHGIPWCGILLDTFTLIVQSSYASRTSRASTF 960

QY 961 NRGFKAGNRBRKLFQVLRKCHSLFLDQVNSLQTVCTNIKILLQAYFPAHCVLQLP 1020
Db 961 NRGFKAGNRBRKLFQVLRKCHSLFLDQVNSLQTVCTNIKILLQAYFPAHCVLQLP 1020

QY 1021 FHQGVKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFL 1080
Db 1021 FHQGVKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFL 1080

Db 1021 FHQGVKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFL 1080
QY 1081 KLTRHRTYVPLIGSLRTAQTOLSRKLPGLTTLALBAANPALPSPFKITLD 1132
Db 1081 KLTRHRTYVPLIGSLRTAQTOLSRKLPGLTTLALBAANPALPSPFKITLD 1132

RESULT 11
US-09-430-323-225
Sequence 225; Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-09-430-323-225

Query Match 99.8%; Score 5952; DB 3; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILSRHYREVLPLATFVRRLGQGNVLVQGDPAFRLVAQCLVCVPM 60
Db 1 MPAPRCRAVRSILSRHYREVLPLATFVRRLGQGNVLVQGDPAFRLVAQCLVCVPM 60

QY 61 DAPPPAASFRVSCLEKELVARVLOQLCEGAKVLAFGPALLGARGPPEAFTTSVR 120

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Db 61 DABPPAPAFRFQVSCIKELVARVQLRCERGAKNVLAFFGALLDARGPPEAFTTSVR 120
Qy 121 SYLPTNTDALARSGAMGLLRVGGDVVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTDALARSGAMGLLRVGGDVVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRGGSASRLPLPRPRR 240
Db 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRGGSASRLPLPRPRR 240
Qy 241 GAAPPEPRTVPGQGSNAHPGRTGSDRGFCVSPAPAEATSLGALSSTHSPSVG 300
Db 241 GAAPPEPRTVPGQGSNAHPGRTGSDRGFCVSPAPAEATSLGALSSTHSPSVG 300
Qy 301 ROHHAQPSSTSRPPRMDTPCPRVYATKHFLLVSSGKXELRSPFLSLRSLTGARRL 360
Db 301 ROHHAQPSSTSRPPRMDTPCPRVYATKHFLLVSSGKXELRSPFLSLRSLTGARRL 360
Qy 361 VETIFLGSRPMPGTPRRLLPRLPQRYWQMRPLFELIGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLLPRLPQRYWQMRPLFELIGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLLVOLLRQHSFMQYGVFVACLRRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLLVOLLRQHSFMQYGVFVACLRRLVPPGLMGS 480
Qy 481 RHERRRLRMTKFTISLGKHAKTSLQELTWMSVDCAMLRSPGVCVPAEHRREEL 540
Db 481 RHERRRLRMTKFTISLGKHAKTSLQELTWMSVDCAMLRSPGVCVPAEHRREEL 540
Qy 541 LAKFLHMSVYVVELLRSPFYVETETTFQKRLFFYRPSVMSLQSIGRQHLKRYQLRE 600
Db 541 LAKFLHMSVYVVELLRSPFYVETETTFQKRLFFYRPSVMSLQSIGRQHLKRYQLRE 600
Qy 601 LSEAENVQHEARPAALTSRLRFLPKPDGLRPIYNDYVVGARTPREKRAEELTGRVKA 660
Db 601 LSEAENVQHEARPAALTSRLRFLPKPDGLRPIYNDYVVGARTPREKRAEELTGRVKA 660
Qy 661 LFSVLYNERARRPGLIGASVLDGDIHRAMRTFVLRAADPPRELYFVAVDTGAYDTI 720
Db 661 LFSVLYNERARRPGLIGASVLDGDIHRAMRTFVLRAADPPRELYFVAVDTGAYDTI 720
Qy 721 POBLTEVIASTIKPQNTYCYRRYAVQKAAHGVRAAFKSHYSTLTLDOPYYKQVAAH 780
Db 721 POBLTEVIASTIKPQNTYCYRRYAVQKAAHGVRAAFKSHYSTLTLDOPYYKQVAAH 780
Qy 781 QETSPLDAAVIEGSSSLNEASSGLFDVFLRFMCHNAVRIRGKSYYCCQIGPGSILSTL 840
Db 781 QETSPLDAAVIEGSSSLNEASSGLFDVFLRFMCHNAVRIRGKSYYCCQIGPGSILSTL 840
Qy 841 LCSTCYGDMENKLFAGIRRDGGLLRVYDVLVPHLTHAKTLRLTVRGVPEYGVNL 900
Db 841 LCSTCYGDMENKLFAGIRRDGGLLRVYDVLVPHLTHAKTLRLTVRGVPEYGVNL 900
Qy 901 RKTYYNPFVEDEALGTAFAVQMPAHGLFPMWCGLLDTRTELEVOSSVYARTSIRASVFP 960
Db 901 RKTYYNPFVEDEALGTAFAVQMPAHGLFPMWCGLLDTRTELEVOSSVYARTSIRASVFP 960
Qy 961 NRGFKAGRNMRKLFVGLRKCHSLFLDLQVNSIQVCTNIYKILLIQAVRFAVCYQLP 1020
Db 961 NRGFKAGRNMRKLFVGLRKCHSLFLDLQVNSIQVCTNIYKILLIQAVRFAVCYQLP 1020
Qy 1021 FHOQWKNPTEFLRVIDSTASLCYSILKAKNAGMSLGAAGAPLBEAOWMCHQAFLL 1080
Db 1021 FHOQWKNPTEFLRVIDSTASLCYSILKAKNAGMSLGAAGAPLBEAOWMCHQAFLL 1080
Qy 1081 KLTHRYTYVPLIGSLRTAQQLSRKLGTTLLTALEAANPALPSDEKTLID 1132
Db 1081 KLTHRYTYVPLIGSLRTAQQLSRKLGTTLLTALEAANPALPSDEKTLID 1132

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RESULT 12

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US-09-128-354-2
; Sequence 2, Application US/09128354
; Patent No. 6337200
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; TITLE OF INVENTION: Genon Corporation
; FILE REFERENCE: 015389-00310US
; CURRENT APPLICATION NUMBER: US/09/128.354
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 08/851,843
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: US 08/854,050
; EARLIER FILING DATE: 1997-05-09
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 09/052,864
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-128-354-2

Query Match 99.8%; Score 5952; DB 3; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPARPCAVNSILSHRYEVLPATFPRRLGPOQMRVLOSADPAAPALVAOCIVCPM 60
Db 1 MPARPCAVNSILSHRYEVLPATFPRRLGPOQMRVLOSADPAAPALVAOCIVCPM 60
Qy 61 DABPPAPAFRFQVSCIKELVARVQLRCERGAKNVLAFFGALLDARGPPEAFTTSVR 120
Db 61 DABPPAPAFRFQVSCIKELVARVQLRCERGAKNVLAFFGALLDARGPPEAFTTSVR 120
Qy 121 SYLPTNTDALARSGAMGLLRVGGDVVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTDALARSGAMGLLRVGGDVVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRGGSASRLPLPRPRR 240
Db 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRGGSASRLPLPRPRR 240
Qy 241 GAAPPEPRTVPGQGSNAHPGRTGSDRGFCVSPAPAEATSLGALSSTHSPSVG 300
Db 241 GAAPPEPRTVPGQGSNAHPGRTGSDRGFCVSPAPAEATSLGALSSTHSPSVG 300
Qy 301 ROHHAQPSSTSRPPRMDTPCPRVYATKHFLLVSSGKXELRSPFLSLRSLTGARRL 360
Db 301 ROHHAQPSSTSRPPRMDTPCPRVYATKHFLLVSSGKXELRSPFLSLRSLTGARRL 360
Qy 361 VETIFLGSRPMPGTPRRLLPRLPQRYWQMRPLFELIGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLLPRLPQRYWQMRPLFELIGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLLVOLLRQHSFMQYGVFVACLRRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLLVOLLRQHSFMQYGVFVACLRRLVPPGLMGS 480

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QY 481 RHNERFLLNTKKTSLGKHALSLQELTWKMSVSDCAMLRRSPGVCPAAEHRLREI 540
DB 481 RHNERFLLNTKKTSLGKHALSLQELTWKMSVSDCAMLRRSPGVCPAAEHRLREI 540
QY 541 LAKFLHMLSVYVVELLRSEFFVYTTETTPQKNLFFRPSVMSKLSIGIRQHLKRVQRE 600
DB 541 LAKFLHMLSVYVVELLRSEFFVYTTETTPQKNLFFRPSVMSKLSIGIRQHLKRVQRE 600
QY 601 LSEAEVRQREARPAALTSRLRFIPKPDGLRPIVMNDYVVGARTREKRAELTSRYKA 660
DB 601 LSEAEVRQREARPAALTSRLRFIPKPDGLRPIVMNDYVVGARTREKRAELTSRYKA 660
QY 661 LFSVLNTERARRRPGLIGASVLTGLDIDHRAMRTFVLRVRAQDPPPELYFKVADVTGAYDTI 720
DB 661 LFSVLNTERARRRPGLIGASVLTGLDIDHRAMRTFVLRVRAQDPPPELYFKVADVTGAYDTI 720
QY 721 PODRLTEVASTIKPONTYCVRRYAVVQKAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
DB 721 PODRLTEVASTIKPONTYCVRRYAVVQKAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
QY 781 QETSPRLDAVLEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSILSLTL 840
DB 781 QETSPRLDAVLEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSILSLTL 840
QY 841 LCSLCYGDMMENKLFAGIRRDGILLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEYGVVNL 900
DB 841 LCSLCYGDMMENKLFAGIRRDGILLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEYGVVNL 900
QY 901 RKTIVNFPVEDALGATAVQMPAHGLFPWCGILLDTPTLEVOSSYSSYASTSRASTF 960
DB 901 RKTIVNFPVEDALGATAVQMPAHGLFPWCGILLDTPTLEVOSSYSSYASTSRASTF 960
QY 961 NRGFKAGRMRRKLFGLVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYEFHACVLOLP 1020
DB 961 NRGFKAGRMRRKLFGLVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYEFHACVLOLP 1020
QY 1021 FHQQVWKNPTFLRVISDTASLCYSILKAKNAGMSLGAAGAAPPSEAVOMLCHQAFLL 1080
DB 1021 FHQQVWKNPTFLRVISDTASLCYSILKAKNAGMSLGAAGAAPPSEAVOMLCHQAFLL 1080
QY 1081 KLTRHRTVTVPLIGSLRTAQOTLSRKLPPTTTALAEANPALPSPDFTIIL 1132
DB 1081 KLTRHRTVTVPLIGSLRTAQOTLSRKLPPTTTALAEANPALPSPDFTIIL 1132

RESULT 13
US-09-675-321-2
; Sequence 2, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-675-321-2

Query Match          99.8%; Score 5952; DB 4; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MPRAPCRARSLLRSHYEVLPATFVRRLPGQWRLOVGGDPAFRALVQICVPM 60
DB 1 MPRAPCRARSLLRSHYEVLPATFVRRLPGQWRLOVGGDPAFRALVQICVPM 60
QY 61 DARPAPAPSFROVSCIKELVAVLQRLCEGAKXVLAEGFALLDGAAGPPEAFTTSVR 120
DB 61 DARPAPAPSFROVSCIKELVAVLQRLCEGAKXVLAEGFALLDGAAGPPEAFTTSVR 120
QY 121 SYLPNTYTDLRSSGAMGLLRVSDVYVHLARALVIVAPSCAYOVCGPPLYQOLA 180
DB 121 SYLPNTYTDLRSSGAMGLLRVSDVYVHLARALVIVAPSCAYOVCGPPLYQOLA 180
QY 181 ATOARPPHNASGPRRLGCEBAMNHSVREAGVPLGLPAFGARRGGASASRLPLPRPBR 240
DB 181 ATOARPPHNASGPRRLGCEBAMNHSVREAGVPLGLPAFGARRGGASASRLPLPRPBR 240
QY 241 GAAPBEPRTVVGQSNAPRGRTGSDRGFCVSPARPBEATSLGALSCTRHPSPVG 300
DB 241 GAAPBEPRTVVGQSNAPRGRTGSDRGFCVSPARPBEATSLGALSCTRHPSPVG 300
QY 301 ROHHAGPSTSRPPRMDTFCPPVYAEYKHFLYSSGDKQLRPSFLLSLRSLTGARL 360
DB 301 ROHHAGPSTSRPPRMDTFCPPVYAEYKHFLYSSGDKQLRPSFLLSLRSLTGARL 360
QY 361 VETIFLGSRPMWGTGRRLLPLRQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPBRAVT 420
DB 361 VETIFLGSRPMWGTGRRLLPLRQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPBRAVT 420
QY 421 PAAGVCAKREKQGSVAAPBEBDTPRRIVOLLROHSPVOYVGFAPACRLRPLPGLMS 480
DB 421 PAAGVCAKREKQGSVAAPBEBDTPRRIVOLLROHSPVOYVGFAPACRLRPLPGLMS 480
QY 481 RHNERFLLNTKKTSLGKHALSLQELTWKMSVSDCAMLRRSPGVCPAAEHRLREI 540
DB 481 RHNERFLLNTKKTSLGKHALSLQELTWKMSVSDCAMLRRSPGVCPAAEHRLREI 540
QY 541 LAKFLHMLSVYVVELLRSEFFVYTTETTPQKNLFFRPSVMSKLSIGIRQHLKRVQRE 600
DB 541 LAKFLHMLSVYVVELLRSEFFVYTTETTPQKNLFFRPSVMSKLSIGIRQHLKRVQRE 600
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DB 601 LSEAEVRQREARPAALTSRLRFIPKPDGLRPIVMNDYVVGARTREKRAELTSRYKA 660
QY 661 LFSVLNTERARRRPGLIGASVLTGLDIDHRAMRTFVLRVRAQDPPPELYFKVADVTGAYDTI 720
DB 661 LFSVLNTERARRRPGLIGASVLTGLDIDHRAMRTFVLRVRAQDPPPELYFKVADVTGAYDTI 720
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DB 721 PODRLTEVASTIKPONTYCVRRYAVVQKAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
QY 781 QETSPRLDAVLEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSILSLTL 840
DB 781 QETSPRLDAVLEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSILSLTL 840
QY 841 LCSLCYGDMMENKLFAGIRRDGILLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEYGVVNL 900
DB 841 LCSLCYGDMMENKLFAGIRRDGILLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEYGVVNL 900
QY 901 RKTIVNFPVEDALGATAVQMPAHGLFPWCGILLDTPTLEVOSSYSSYASTSRASTF 960
DB 901 RKTIVNFPVEDALGATAVQMPAHGLFPWCGILLDTPTLEVOSSYSSYASTSRASTF 960
QY 961 NRGFKAGRMRRKLFGLVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYEFHACVLOLP 1020
DB 961 NRGFKAGRMRRKLFGLVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYEFHACVLOLP 1020
QY 1021 FHQQVWKNPTFLRVISDTASLCYSILKAKNAGMSLGAAGAAPPSEAVOMLCHQAFLL 1080
DB 1021 FHQQVWKNPTFLRVISDTASLCYSILKAKNAGMSLGAAGAAPPSEAVOMLCHQAFLL 1080

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Tue Dec 21 15:43:30 2004

us-08-974-584c-118.rat

Page 15

QY 1081 KLTRHRTVYVLLGSRLTAQTO:SRKLPCTTLTALBAAANPALPSDFKILD 1132
Db 1081 KLTRHRTVYVLLGSRLTAQTO:SRKLPCTTLTALBAAANPALPSDFKILD 1132

RESULT 14

US-09-052-919-2

Sequence 2, Application US/9052919

Patent No. 6444650

GENERAL INFORMATION:

APPLICANT: Czech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin B.

APPLICANT: Andrews, William H.

TITLE OF INVENTION: Antisense Compositions for Detecting and

INHIBITING Telomerase Reverse Transcriptase

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/052,919

FILING DATE: 31-MAR-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/974,549

FILING DATE: 19-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/974,584

FILING DATE: 19-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

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REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-052-919-2

Query Match 99.8%; Score 5952; DB 4; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPBARCAVYVSLRSHYREVLPATFRRRLPGQGMRLVORGDPAAPALVAOCLVCPM 60
Db 1 MPBARCAVYVSLRSHYREVLPATFRRRLPGQGMRLVORGDPAAPALVAOCLVCPM 60
QY 61 DARPPAPSFROYSCLELYAVYLOLCERGANVLAFGALIDGARGPPEAFTTSVR 120
Db 61 DARPPAPSFROYSCLELYAVYLOLCERGANVLAFGALIDGARGPPEAFTTSVR 120
QY 121 SYLPTVTVDALRGSGAMGLLRVYDDVYLHLLARCALFYVARSQAYVCGPPLVYQGA 180
Db 121 SYLPTVTVDALRGSGAMGLLRVYDDVYLHLLARCALFYVARSQAYVCGPPLVYQGA 180
QY 181 ATQAPPPHAGSPRRRLCERAMNHSVEAGVPLGPAPGARRGSGASRSLPLPKPRR 240
Db 181 ATQAPPPHAGSPRRRLCERAMNHSVEAGVPLGPAPGARRGSGASRSLPLPKPRR 240
QY 241 GAAPPERTPVQGGSWAHGRTGSDRGFCVSPAPAEATSLGALSCTRSHSPSVG 300
Db 241 GAAPPERTPVQGGSWAHGRTGSDRGFCVSPAPAEATSLGALSCTRSHSPSVG 300
QY 301 ROHNGPSTSRPPPMPTPCPPYAEFRHFLYSGDGEOLRPSFLSLRPSLTGARL 360
Db 301 ROHNGPSTSRPPPMPTPCPPYAEFRHFLYSGDGEOLRPSFLSLRPSLTGARL 360
QY 361 VETIFLGRPMWPGTFRRLPLRQRYWOMRPLFELLGNHACPEYVLLKTHCPRAAVT 420
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QY 421 PAAGVCAREKPOGVAAPSEEDTDPRRLVOLLRQSSSWQYGVFRACLRLLVPGLMGS 480
Db 421 PAAGVCAREKPOGVAAPSEEDTDPRRLVOLLRQSSSWQYGVFRACLRLLVPGLMGS 480
QY 481 RHNERFLRNTKKFSLGKAKLSTLOELTWKSYVDCAMLRSPDVGCVPAEARELRREI 540
Db 481 RHNERFLRNTKKFSLGKAKLSTLOELTWKSYVDCAMLRSPDVGCVPAEARELRREI 540
QY 541 LAKFLHMTMSYVVELLSFFVYVETTFQKRLFFRYRSVWSKOSIGIRQHLKRVQRE 600
Db 541 LAKFLHMTMSYVVELLSFFVYVETTFQKRLFFRYRSVWSKOSIGIRQHLKRVQRE 600
QY 601 LSEAEVRQHREARPPALTSRLRFIPKPGGLRPIVMDVYVAGARTFRERKARELTSRYKA 660
Db 601 LSEAEVRQHREARPPALTSRLRFIPKPGGLRPIVMDVYVAGARTFRERKARELTSRYKA 660
QY 661 LFSVINYERARRPGLLGASVIGLDDIHRAMTFVIRVAQDPPELRYKVDVTGAYDTI 720
Db 661 LFSVINYERARRPGLLGASVIGLDDIHRAMTFVIRVAQDPPELRYKVDVTGAYDTI 720
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Db 721 PODRLTEVIASIKQNTYCVRYAVVQKAHGHYKAFKSHVSTLTLOLYMROFVHL 780
QY 781 QETSPLRDAVYIEQSSSLNEASGLFDFELRMCHAVRIKSGSYVQCGIIPQGSILSTL 840
Db 781 QETSPLRDAVYIEQSSSLNEASGLFDFELRMCHAVRIKSGSYVQCGIIPQGSILSTL 840

QY 841 LSLCYGCMENKLFAGIRDDGLLLVDDFLVTHLTHAKTFLTLVRCVPEYCVNL 900
DB 841 LSLCYGCMENKLFAGIRDDGLLLVDDFLVTHLTHAKTFLTLVRCVPEYCVNL 900
QY 901 KTVVNFPEVDALGCTAVQMPAHGLPFGCLLDPTRTLEVQSYSSVARTSRASVTF 960
DB 901 KTVVNFPEVDALGCTAVQMPAHGLPFGCLLDPTRTLEVQSYSSVARTSRASVTF 960
QY 961 NRGFKAGNRMRKLFVGLRLKCHSLFDLQVNSLQVCTNIVKILLQVRFHACVGLP 1020
DB 961 NRGFKAGNRMRKLFVGLRLKCHSLFDLQVNSLQVCTNIVKILLQVRFHACVGLP 1020
QY 1021 FHQOVKNGNTEFLRYISDPAAS-CYSILKAKXAGSLKGAAGPSPSAVOMLCHQAFLL 1080
DB 1021 FHQOVKNGNTEFLRYISDPAAS-CYSILKAKXAGSLKGAAGPSPSAVOMLCHQAFLL 1080
QY 1081 KLTRHRYTVPLGLSLRINQVLSRKLPGTTLVTALEAANPALPSDFKTIID 1132
DB 1081 KLTRHRYTVPLGLSLRINQVLSRKLPGTTLVTALEAANPALPSDFKTIID 1132

RESULT 15
US-08-912-951-2
Sequence 2, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-2

Query Match 99.8%; Score 5952; DB 4; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRLPPQGRVLVQRGDPAAFRLVAQCLVCPM 60
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRLPPQGRVLVQRGDPAAFRLVAQCLVCPM 60
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DB 61 DAPPPAABSFROVSCLELVARVYLQRCERAKVLAFFGRLLDGARGPPEAFTTSVR 120
QY 121 SYLPNTVDALRGSGAMGLLRVGGDVLVHLASGALFVLVAPSCAVOCCPPLYOLGA 180
DB 121 SYLPNTVDALRGSGAMGLLRVGGDVLVHLASGALFVLVAPSCAVOCCPPLYOLGA 180
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DB 181 ATQARPPEASGRRRLGCERAMNHSVREAGVPLGIPAGARRGGSASRSILPXPERR 240
QY 241 GAAPPEERTPVQGSVAHAGRTGSPDRGFCVSPAPRAPEEATSLGALSGRHHSPVG 300
DB 241 GAAPPEERTPVQGSVAHAGRTGSPDRGFCVSPAPRAPEEATSLGALSGRHHSPVG 300
QY 301 RQHAGPSTSPRPAPWDTPCPVYAETGHPYSSGDKQLRPSFLSLRPSLTGARRL 360
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DB 361 VETIFGSRPMWGPTRRLPLPORYWQRPPLFELIGNHAOCPPVYLKTKCPRAVT 420
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DB 421 PAAGVCAKPKQGSVAAPREEDTDPRLVQLRQHSPPQVGYFRACTRLVPPGLWS 480
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DB 481 RANRRFLNNTKFKISLGGAKLSLOELTWKSVVDCAMLRSPGVGCYPAAEHRLREBI 540
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DB 541 LAKELHMLSVYVVELRSPFYVTETTPQKNLFFYPSPVMSKLSIGIRQHLKXVOLRE 600
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DB 661 LPSVLYNERARRPGLLGASVGLDIDIRAWRFVLRVRAQDDPPLYPFKVUDVATYTI 720
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DB 721 PODRLTEVATSIKPPONTCVARYAVVQKAAGHYRKAFFKSHVSTLTDLPYMRQFVAHL 780
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Db 781 QETSPRLDAVIEQSSSLNEASSGLFDVFLRFMCHAVIRIGSKSYVCCGIPQGSILSTL 840
QY 841 LGLSLCIGDMENKLFAGIRRDGLLRLVYDDDLVTPHITAKTFLRLVNGVPEYGVVNL 900
Db 841 LGLSLCIGDMENKLFAGIRRDGLLRLVYDDDLVTPHITAKTFLRLVNGVPEYGVVNL 900
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Db 901 RKTIVNPFVEDELGLTAFVQMPAHGLFPWCGILLDTRTEVQSDYSVARTIRASVTF 960
QY 961 NRGFKAGRMNRKLFVYLRLKCHSLFLDLQVNSLQVCTNIVKILLQAVRPHACVLQIP 1020
Db 961 NRGFKAGRMNRKLFVYLRLKCHSLFLDLQVNSLQVCTNIVKILLQAVRPHACVLQIP 1020
QY 1021 FHOQWKNPTEFRLVISTASLCSYILIKAKNAGMSIGAKGAGPLPSEAVQWLCHQAFIL 1080
Db 1021 FHOQWKNPTEFRLVISTASLCSYILIKAKNAGMSIGAKGAGPLPSEAVQWLCHQAFIL 1080
QY 1081 KLTFRHRTVYVLLGSLRTAQTOLSRKLPCTTLTALLEANPALPSDKTILD 1132
Db 1081 KLTFRHRTVYVLLGSLRTAQTOLSRKLPCTTLTALLEANPALPSDKTILD 1132

RESULT 16
US-09-402-181B-2
Sequence 2, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:

NAME: Aisenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-0026200S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-402-181B-2

Query Match 99.8%; Score 5952; DB 4; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPARPCRAVRSILRSHYREVLPLATEFYRLGPQGMRLVQGDPAFAFALVAQCLVCPW 60
Db 1 MPARPCRAVRSILRSHYREVLPLATEFYRLGPQGMRLVQGDPAFAFALVAQCLVCPW 60
QY 61 DARPPAAPSTROYSCLEKELVAVYLQRLCERGANVLAFGALLDGAAGGPEAFITSVR 120
Db 61 DARPPAAPSTROYSCLEKELVAVYLQRLCERGANVLAFGALLDGAAGGPEAFITSVR 120
QY 121 SYLPNTVTDALRGSGAMGLLRVYGDVYLVAHLARCALFVLVAPSCAYQVGGPPLYOLGA 180
Db 121 SYLPNTVTDALRGSGAMGLLRVYGDVYLVAHLARCALFVLVAPSCAYQVGGPPLYOLGA 180
QY 181 ATQARPPHAGSPRRRLICERAMNHSYAEAGVPLGLPAPGARRGSGASRSPLPKSPRR 240
Db 181 ATQARPPHAGSPRRRLICERAMNHSYAEAGVPLGLPAPGARRGSGASRSPLPKSPRR 240
QY 241 GAAPPERTPVQGSMAHPRGTRGSDRGFCVSPAPAEATSLGALSTRSHPSVG 300
Db 241 GAAPPERTPVQGSMAHPRGTRGSDRGFCVSPAPAEATSLGALSTRSHPSVG 300
QY 301 RQHNAGPSTSRPRPMDTPCPVYAEIKHFLYSSGDKQULPSFLSLSPSTLGARL 360
Db 301 RQHNAGPSTSRPRPMDTPCPVYAEIKHFLYSSGDKQULPSFLSLSPSTLGARL 360
QY 361 VETITLSRPPMPCGTPRLPLPQRYWQMRPLFELLGNHACQCYGVLLKTHCGLRAVT 420
Db 361 VETITLSRPPMPCGTPRLPLPQRYWQMRPLFELLGNHACQCYGVLLKTHCGLRAVT 420
QY 421 PAAGCAHEKPOGSAABEEDTPRRLVQLRHSSHWQYGVFVACRLVPPGLMGS 480
Db 421 PAAGCAHEKPOGSAABEEDTPRRLVQLRHSSHWQYGVFVACRLVPPGLMGS 480
QY 481 RHNERRFLRNTKKTISLQKHAHSLQELTWKSVYDCAHLRSPGVGCVPAEHLREBI 540
Db 481 RHNERRFLRNTKKTISLQKHAHSLQELTWKSVYDCAHLRSPGVGCVPAEHLREBI 540
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Db 541 LAKFLHMTMSVYVVELLSFFVYMETFOKRLTFEYPSVSKXOSIGIRHLLRVQRE 600
QY 601 LSEAEVRQREBARPALTSRLRFLPKDGLAPIVNMDVVGARTFRREKRAERLTSRYKA 660
Db 601 LSEAEVRQREBARPALTSRLRFLPKDGLAPIVNMDVVGARTFRREKRAERLTSRYKA 660
QY 661 LFSVINYRARRPGLGASVGLDIDIRAWTFTLRRRAQDPPPELTFVKADVGAADTI 720
Db 661 LFSVINYRARRPGLGASVGLDIDIRAWTFTLRRRAQDPPPELTFVKADVGAADTI 720
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Db 721 PODRLTEVIASIIIPONTYCVRRYAVVQKAAHGVKAFKSHVSTLTDLPYMQFVAHL 780
QY 781 QETSPRLDAVIEQSSSLNEASSGLFDVFLRFMCHAVIRIGSKSYVCCGIPQGSILSTL 840

Db 781 OETSPRDVAVIEOSSSINEASSGLDFVLRPMCHAVRIGKSYVOCQIGPQSIISLTL 840
 Qy 841 LSLCYGDMENLFGIRRDGLLRLVDFPLVTPHLTHAKTFLRTLVGVPEYGVNL 900
 Db 841 LSLCYGDMENLFGIRRDGLLRLVDFPLVTPHLTHAKTFLRTLVGVPEYGVNL 900
 Qy 901 KRTVNFPEDEALGTAFCVMPAHGLPFWCGLLDPTLEVOYSSYARTSIRASLTF 960
 Db 901 KRTVNFPEDEALGTAFCVMPAHGLPFWCGLLDPTLEVOYSSYARTSIRASLTF 960
 Qy 961 NNGFKAGRMRRKLGVLRLKCHSLFLDLQVNSLQVCTNLYKILLQAYFFHACVLOLP 1020
 Db 961 NNGFKAGRMRRKLGVLRLKCHSLFLDLQVNSLQVCTNLYKILLQAYFFHACVLOLP 1020
 Qy 1021 PHQOVKNPTFPLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080
 Db 1021 PHQOVKNPTFPLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080
 Qy 1081 KLTRRVTYVPLGLSRTAQQLSRKLTGTTTLTALEANALPBDFTIIL 1132
 Db 1081 KLTRRVTYVPLGLSRTAQQLSRKLTGTTTLTALEANALPBDFTIIL 1132

RESULT 17

US-09-721-456-2
 Sequence 2, Application US/09721456

Patent No. 6617110
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Langer, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Hatley, Calvin B.
 Andrews, William B.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,456
 FILING DATE: 22-NOV-1997
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17685
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-721-456-2

Query Match 99.8%; Score 5952; DB 4; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSILRSHREVLPATFVRLPGQGRVLYQGDPAAPRALVAQCLVCPM 60
 Db 1 MPAPRCRAVRSILRSHREVLPATFVRLPGQGRVLYQGDPAAPRALVAQCLVCPM 60
 Qy 61 DARPAPAAAPROVSCLELVARVQLRCEKRAKVNLAAGFALLDGAAGCPREARTSVR 120
 Db 61 DARPAPAAAPROVSCLELVARVQLRCEKRAKVNLAAGFALLDGAAGCPREARTSVR 120
 Qy 121 SYLPTVTDALRSGAGMLLRVGDVYVHLAACAFLVLAAPSCAYVCCPPLVYOLGA 180
 Db 121 SYLPTVTDALRSGAGMLLRVGDVYVHLAACAFLVLAAPSCAYVCCPPLVYOLGA 180
 Qy 181 ATQARPPIASGRRRLGGERAMNHSVREAGVPLGIPAPGARRGSGASRSILPLKRRPR 240
 Db 181 ATQARPPIASGRRRLGGERAMNHSVREAGVPLGIPAPGARRGSGASRSILPLKRRPR 240
 Qy 241 GAAPBEERTPVGGSAHAGTRGSDRGCVVSPAPAPAEATSLGALSGTRHSPSYG 300
 Db 241 GAAPBEERTPVGGSAHAGTRGSDRGCVVSPAPAPAEATSLGALSGTRHSPSYG 300
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 Db 361 VETIFGSRPMPGTRRLPLPQRYWQMRPLFELLGHAACCPGVLLKTCPLRAAVT 420
 Qy 421 PAAGVCAKPKPGSVAPAEEDTDPRRLVQLRQHSFPQVYGFYRACLRLLVPPGLMGS 480
 Db 421 PAAGVCAKPKPGSVAPAEEDTDPRRLVQLRQHSFPQVYGFYRACLRLLVPPGLMGS 480
 Qy 481 RHNERPFLNRTKKEFISLGHAKLSLOELTWKQSVRDCAMLRSPGVGYPALEHRLREI 540
 Db 481 RHNERPFLNRTKKEFISLGHAKLSLOELTWKQSVRDCAMLRSPGVGYPALEHRLREI 540
 Qy 541 LAKFLHMLSVYVELLRSFYVTEETFOKNRLFYRFPVWVKLOSIGIRQLKKEVQRE 600
 Db 541 LAKFLHMLSVYVELLRSFYVTEETFOKNRLFYRFPVWVKLOSIGIRQLKKEVQRE 600
 Qy 601 LSAEVRQREARFALLTSRLRPIPKPDGLPIVMDVYVGAARTRRERARLTSRYVA 660
 Db 601 LSAEVRQREARFALLTSRLRPIPKPDGLPIVMDVYVGAARTRRERARLTSRYVA 660
 Qy 661 LPSVLYNERARPGILGASVGLGDIHRAMRFVLRVRODPPPELYPKVVTGAYDTI 720
 Db 661 LPSVLYNERARPGILGASVGLGDIHRAMRFVLRVRODPPPELYPKVVTGAYDTI 720
 Qy 721 PQRRLTEVIAIIPONTYCVRRYAVVQRAAGHAKAKFSVSTLTLDIOPYRQFVAHL 780

Db 721 PODRLTEVIAIISKQNTYCVRRYAVVQKAAGHVAKAFKSHVSTLTLDQPMRQFVAHL 780
Qy 781 QETSPLEDAVITESSSLINASSGLFVFLRFMKHNAVIRKGSYVOCQIGQSIITSL 840
Db 781 QETSPLEDAVITESSSLINASSGLFVFLRFMKHNAVIRKGSYVOCQIGQSIITSL 840
Qy 841 LCLSLCYDMENKLFAGIRRDGLRLVDDFLVPLTHAKTFLRLTVRGVPEYGVNL 900
Db 841 LCLSLCYDMENKLFAGIRRDGLRLVDDFLVPLTHAKTFLRLTVRGVPEYGVNL 900
Qy 901 RKTIVNPFVDEALGTAFAVQMPAHGLFPMCGILDTRTLLEVOSSVARTSIRASVTF 960
Db 901 RKTIVNPFVDEALGTAFAVQMPAHGLFPMCGILDTRTLLEVOSSVARTSIRASVTF 960
Qy 961 NRGFKAGNRMRKLFVYLKCHSLFLDLQVNSIQVCTNIYKILLQAFRFAVQLQIP 1020
Db 961 NRGFKAGNRMRKLFVYLKCHSLFLDLQVNSIQVCTNIYKILLQAFRFAVQLQIP 1020
Qy 1021 FHOQVKNPTEFLRVISDTASLQVSIILKAKNAGMSIGAKGAPLSEAVQWLCHQAFLL 1080
Db 1021 FHOQVKNPTEFLRVISDTASLQVSIILKAKNAGMSIGAKGAPLSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTVPLJGSLRTAQTQSRKLPSTTLTALLEANPALPSDFKTLTD 1132
Db 1081 KLTRHRVTVPLJGSLRTAQTQSRKLPSTTLTALLEANPALPSDFKTLTD 1132

RESULT 18
US-09-953-052-2
Sequence 2' Application US/09953052
Patent No. 6627619
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,052
FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: MO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: MO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2

Query Match 99.8% Score 5952; DB 4; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MPAPRCRAVSLRSHREVLPLATFVRLGPGQWLVQGRDPAFAFALVACVCPW 60
Db 1 MPAPRCRAVSLRSHREVLPLATFVRLGPGQWLVQGRDPAFAFALVACVCPW 60
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Db 61 DARPAPAPSFROYSCLELVARVQLRCERAGKAVLAFGALLDDGARGPPEAFTTSVR 120
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Db 121 SYLPNTVDAIRGGAGWLLLRVGDVYLHLARCALFVLVAPSCAYQVGPPLYQCHA 180
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Db 181 ATQAPPPHAGSPRRRLCCERAMNHSVEAGVPLGLPAPGARRRGASASRLPIPKRRR 240
Qy 241 GAAPPERTPVGQGMWHPGRTGSPDRGFCVSPAPAPAEATSLGALSTGRSHPSVG 300
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Qy 421 PAAGVCAEKPOGSAAPBEEDTDPRLVOLLROHSSPMQVYGFVRAICLRILVPPGLMS 480
Db 421 PAAGVCAEKPOGSAAPBEEDTDPRLVOLLROHSSPMQVYGFVRAICLRILVPPGLMS 480
Qy 481 RHNRRLPLRNTKRLISLGAKLSLQSLTYMKSGTRDQMLRRSGVGVCPAAERLREBI 540
Db 481 RHNRRLPLRNTKRLISLGAKLSLQSLTYMKSGTRDQMLRRSGVGVCPAAERLREBI 540
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Db 541 LAKFLHMLMSVYVELLSFFVYETTFQKNRLFFYPSPVMSKLSIGIRQLRVLQRE 600
Qy 601 LSEAENVQHRAPALLTSRLRFLPKPDGLRPIVNDYVVGARTFRREKAEERLTSVKA 660
Db 601 LSEAENVQHRAPALLTSRLRFLPKPDGLRPIVNDYVVGARTFRREKAEERLTSVKA 660

QY 661 LFSVLYNERARRPGLGLGASVILGLDIDHRAWRTPVLEVRADPPPELYFVKVDTGAVDTI 720
 DB 661 LFSVLYNERARRPGLGLGASVILGLDIDHRAWRTPVLEVRADPPPELYFVKVDTGAVDTI 720
 QY 721 FQDRLETVIATIKQNTYCVRRVAVVQKAHGHVRKAFKSHVSTLTDLDQYMGQFVAHL 780
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 DB 841 LQSLCYGDMENKLFAGIRRDGILLRLVDDFLVLTPLTHAFTPLTLVRSVPEYGVNLT 900
 QY 901 RKTVMNFPEDBALGTAFCVQMPAHGLFPWCGILLDTLRTLEVSQSYSTASTIRASVTF 960
 DB 901 RKTVMNFPEDBALGTAFCVQMPAHGLFPWCGILLDTLRTLEVSQSYSTASTIRASVTF 960
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 DB 961 NRGFKAGNRMRKRLFGVLRKLSLFLDLQVNSLQTVCTNITYKILLQAYEFHACVQLP 1020
 QY 1021 FHQQWKNFTFPLRYISDTASLCYSILKAKNAGMSLGAKGAGPLPSAVQWMLCHQAFLL 1080
 DB 1021 FHQQWKNFTFPLRYISDTASLCYSILKAKNAGMSLGAKGAGPLPSAVQWMLCHQAFLL 1080
 QY 1081 KTRRRVTVPLGLSLRTAQTOLSRKLPQTTLTALAANPALPSDFKTIID 1132
 DB 1081 KTRRRVTVPLGLSLRTAQTOLSRKLPQTTLTALAANPALPSDFKTIID 1132

RESULT 19
 US-09-042-460-3
 Sequence 3, Application US/09042460
 Patent No. 6767719
 GENERAL INFORMATION:
 APPLICANT: Morin, Gregg B.
 APPLICANT: Allsopp, Richard
 APPLICANT: Depinto, Ronald
 APPLICANT: Greenberg, Roger
 TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase
 NUMBER OF SEQUENCES: 101
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/042,460
 FILING DATE: 16-MAR-1998
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/974,549
 FILING DATE: 19-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/974,584
 FILING DATE: 19-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/979,742
 FILING DATE: 26-NOV-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Einhorn, Gregory P.
 REGISTRATION NUMBER: 38,440
 REFERENCE/DOCKET NUMBER: 015389-003110US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ. ID NO. 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1132
 OTHER INFORMATION: /note="human telomerase reverse
 OTHER INFORMATION: transcriptase (hTERT)"
 US-09-042-460-3

Query Match 99.8%; Score 5952; DB 4; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPAPRCRAVRSILRSYREVLPATFVRRLGFGWRILVQGDPAARFALVAQCLVCVW 60
 DB 1 MPAPRCRAVRSILRSYREVLPATFVRRLGFGWRILVQGDPAARFALVAQCLVCVW 60
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 DB 61 DABPPPAASFROYSCIKELVAVVLQRLCERGAKNVLAAGFALLDARGGPPAFTSVR 120
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 DB 121 SYLPNTVTDALRSGAGMLLRVGDVVLHLLARCALFVLVAPSCAYVCGPFLYOLGA 180
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 DB 241 GAAPPEPRTVGGSNANPGRTRGPDRCGVVSPARPAEATSLGALSGTRHSPSVG 300
 QY 301 RGHAGPPTSRPPRPWTPTCPVVAETKXFIYSSGDKQLRPSFLLSLRPSLTGARRL 360


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Db 301 ROHAGSPSTSRPPMDTDCPPVYABTKFLVSSGDKEDLRPSFLISSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPTGPRRLPRLPORVQWMPPLFELIGNAOCQYGVLLKTHCPRAVY 420
Db 361 VETIFLGSRRPMPTGPRRLPRLPORVQWMPPLFELIGNAOCQYGVLLKTHCPRAVY 420
Qy 421 PAACVACREKQGSVAAPBEEDTDPRRLVOLLRQHSPPWQYGVFVRACLRVLVPGIWS 480
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Db 541 LAKELHMLMSVYVVELLRSPFYVTEETFOKNRLEFYRPSVSKLQSIGRQHLKRVQRE 600
Qy 541 LAKELHMLMSVYVVELLRSPFYVTEETFOKNRLEFYRPSVSKLQSIGRQHLKRVQRE 600
Db 541 LAKELHMLMSVYVVELLRSPFYVTEETFOKNRLEFYRPSVSKLQSIGRQHLKRVQRE 600
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Db 661 LFSVLYNERARRPGLLGASVGLDDIHRAMRTFYLVRADPPPELYFYVAVDTGAYDTI 720
Qy 721 PODRLTEVIAIIRPQNTYCYRRAVYQKAAGHVRAKAFSHVSTLTDLPYKQRYAHL 780
Db 721 PODRLTEVIAIIRPQNTYCYRRAVYQKAAGHVRAKAFSHVSTLTDLPYKQRYAHL 780
Qy 781 QETSPLDVAVIEOSSSLNEASSGLFVPLRFEMCHAVRIRGKSYVQCGIIPGSLITSL 840
Db 781 QETSPLDVAVIEOSSSLNEASSGLFVPLRFEMCHAVRIRGKSYVQCGIIPGSLITSL 840
Qy 841 LCSLCYGDMENKLPAGIRRDGLLRJVDLFLVPLTHAKTFLRLVAGVPEYGVNL 900
Db 841 LCSLCYGDMENKLPAGIRRDGLLRJVDLFLVPLTHAKTFLRLVAGVPEYGVNL 900
Qy 901 RKTVMNFEVDEALGTAFAVQMPAHGLFPWCGILLDRTEVSDVSRYRTIRASVTF 960
Db 901 RKTVMNFEVDEALGTAFAVQMPAHGLFPWCGILLDRTEVSDVSRYRTIRASVTF 960
Qy 961 NRGEKAGRNRRKLPFVLRKCHSLFLDQVNSLQVCTNIYKILLDQAVRFACVQLP 1020
Db 961 NRGEKAGRNRRKLPFVLRKCHSLFLDQVNSLQVCTNIYKILLDQAVRFACVQLP 1020
Qy 1021 FHQQWKNPFFFLRVISDTSLCYSLIKAKNAQMSLGAKAAGPLDSEAVQWLC HQAFLL 1080
Db 1021 FHQQWKNPFFFLRVISDTSLCYSLIKAKNAQMSLGAKAAGPLDSEAVQWLC HQAFLL 1080
Qy 1081 KLTRHRVTVPLIGSLRTAQTOLSRKLPCTTLTALANAANPALPSPFKITLD 1132
Db 1081 KLTRHRVTVPLIGSLRTAQTOLSRKLPCTTLTALANAANPALPSPFKITLD 1132

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RESULT 20
US-08-974-549A-611
/ Sequence 611, Application US/08974549A
/ Patent No. 6166178
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Hawley, Calvin B.
/ APPLICANT: Andrews, William H.
/ TITLE OF INVENTION: Human telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor

```

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/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/974,549A
/ FILING DATE: 19-NOV-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-OCT-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 611:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1154 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Protein
/ LOCATION: 1..1154
/ OTHER INFORMATION:
/ OTHER INFORMATION: /note= "fusion protein composed of hTERT
/ protein sequence, vector sequences, the
/ MYC epitope and His6 tag"
US-08-974-549A-611

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Qy 1 MPBAPRCRAVSLLSRSHREVLPATFVRLPGQGMRLVQGDPAFPAALVAQCLVCPW 60
Db 1 MPBAPRCRAVSLLSRSHREVLPATFVRLPGQGMRLVQGDPAFPAALVAQCLVCPW 60
Query Match 99.8% Score 5952; DB 3; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 61 DARPAPABSFQVSCLELVAVIQLCERGAKNVLAFFGALLDGAAGPPEAFTTSVR 120
DB 61 DARPAPABSFQVSCLELVAVIQLCERGAKNVLAFFGALLDGAAGPPEAFTTSVR 120
QY 121 SYLPTVTDALRGSGMGLLRVGDVYLHLACALFVLVAPSCAQVCGPPLYOGA 180
DB 121 SYLPTVTDALRGSGMGLLRVGDVYLHLACALFVLVAPSCAQVCGPPLYOGA 180
QY 121 SYLPTVTDALRGSGMGLLRVGDVYLHLACALFVLVAPSCAQVCGPPLYOGA 180
DB 121 SYLPTVTDALRGSGMGLLRVGDVYLHLACALFVLVAPSCAQVCGPPLYOGA 180
QY 181 ATOAAPPPHASPBRRLGGERAMNHSVRBAGVPLCLPAPGARRGGSASRLPLPKPRR 240
DB 181 ATOAAPPPHASPBRRLGGERAMNHSVRBAGVPLCLPAPGARRGGSASRLPLPKPRR 240
QY 241 GAAPBERTPVGGGSAHAPGRTRGSDGFCVVSAPABEATSLGALSGTRSHSPVSG 300
DB 241 GAAPBERTPVGGGSAHAPGRTRGSDGFCVVSAPABEATSLGALSGTRSHSPVSG 300
QY 301 ROHHAAPBSTSRPPRMDTCCPVYAETGHLVSSGDKQLRPSLTLSPSLTGARL 360
DB 301 ROHHAAPBSTSRPPRMDTCCPVYAETGHLVSSGDKQLRPSLTLSPSLTGARL 360
QY 361 VETIFGSRPMWPGTPRRPLPRLPORYWQMRPLFLLGNHOCPCYVLLKTHCPRAVT 420
DB 361 VETIFGSRPMWPGTPRRPLPRLPORYWQMRPLFLLGNHOCPCYVLLKTHCPRAVT 420
QY 421 PAAGVCAKPKPGSVAAPEEDTDPRRLVQLRQHSPPWQYGFYACLRRLVPGGLWS 480
DB 421 PAAGVCAKPKPGSVAAPEEDTDPRRLVQLRQHSPPWQYGFYACLRRLVPGGLWS 480
QY 481 RHNERFLNNTKKFISLGHAKLSLOELTWKNSVDCAMLRSPGVGCPAAEHRLREI 540
DB 481 RHNERFLNNTKKFISLGHAKLSLOELTWKNSVDCAMLRSPGVGCPAAEHRLREI 540
QY 541 LAKFLHMLMSVYVELLSFFVYVTEETFOKNLFFYRPSVMSKLOSIGRHLKRVQRE 600
DB 541 LAKFLHMLMSVYVELLSFFVYVTEETFOKNLFFYRPSVMSKLOSIGRHLKRVQRE 600
QY 601 LSEAEVQREARPAALLTSRLRFFIKPDGLPIVNDYVVGARTFRKKAERLTSRYKA 660
DB 601 LSEAEVQREARPAALLTSRLRFFIKPDGLPIVNDYVVGARTFRKKAERLTSRYKA 660
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DB 661 LSVLNVKEARPPGLIGASVGLDIDIRHMRTEFVRVAODPPPLVYKVDVGAVTI 720
QY 721 PODRLTEVIAIIPONTVCVRVAVVQKAAHGHYKAKFKSHVSTLTDLOPYMRQFAHL 780
DB 721 PODRLTEVIAIIPONTVCVRVAVVQKAAHGHYKAKFKSHVSTLTDLOPYMRQFAHL 780
QY 781 OETSPLRDAVVIQOSSSLNEASSGLFDVFLRMCHHAARIRKGSVVOCGIPOGSIISL 840
DB 781 OETSPLRDAVVIQOSSSLNEASSGLFDVFLRMCHHAARIRKGSVVOCGIPOGSIISL 840
QY 841 LGSICGDMENKLFAGIRDGLLRLVDDFLVTHLTAKTFLRTLVRGVEYCVVNL 900
DB 841 LGSICGDMENKLFAGIRDGLLRLVDDFLVTHLTAKTFLRTLVRGVEYCVVNL 900
QY 901 RKTVPNFPVEDEALGTAFAVQMPAGLFPWCGLLDTRLEVOQSYSSARISASLTF 960
DB 901 RKTVPNFPVEDEALGTAFAVQMPAGLFPWCGLLDTRLEVOQSYSSARISASLTF 960
QY 961 NRGFKAGRMRRRLFGVLRKCHSLFLDQVNSLQVCNIXKILLQAYRHAQVLDLP 1020
DB 961 NRGFKAGRMRRRLFGVLRKCHSLFLDQVNSLQVCNIXKILLQAYRHAQVLDLP 1020
QY 1021 FHQQVKNPFFLRLVISTASLCSYLKAKNAGMSIGAKGAGPLPSEAVQNLCHQAFLL 1080
DB 1021 FHQQVKNPFFLRLVISTASLCSYLKAKNAGMSIGAKGAGPLPSEAVQNLCHQAFLL 1080
QY 1081 KLTRHVVYVPLIGSLRTAQOLSRLLBCTTTLTALAANPALPBDPFTIIL 1132
DB 1081 KLTRHVVYVPLIGSLRTAQOLSRLLBCTTTLTALAANPALPBDPFTIIL 1132

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RESULT 21
US-08-912-951-323
; Sequence 323, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Linsner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Hatley, Calvin H.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-Aug-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-May-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-May-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 18-Apr-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-Oct-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 323:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-323
Query March 99.8%; Score 5952; DB 4; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
1 MPRAPRCAVRSILRSYREVVLATFVRLGQGRVVGQBPAPAFALVNAQIVCPW 60

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Db 1 MPBAPCRVAVSLRSHYREVLPATFVRLRGQKWLVRGDPBAFPAFVAQCLVCPW 60
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Db 61 DAPPAPAPSFROVSCIKELVAVLQRLCERGAKNVLAQFALLDQAGCPPEAFTTSVR 120
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Db 121 SYLPNTVTDLRGSGMGILLRVRGDDVYVHLARCALPVLVAPSCAYOCCPEPLQLA 180
Qy 181 ATQARPPHAGSRRRLGGERAMNHSYREAGVPLGLPAPGARRGGSASRLPFRPRR 240
Db 181 ATQARPPHAGSRRRLGGERAMNHSYREAGVPLGLPAPGARRGGSASRLPFRPRR 240
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Db 241 GAAPERTPTVGGGSAHNPRTGSPRGCVVSPAPAPAEATSLGALSGTHSHPSVG 300
Qy 301 ROHHAGPSTSRPPRPMPTCPVVAETKHFLLYSSGCKEQLRPSFLSLRPSLTGARL 360
Db 301 ROHHAGPSTSRPPRPMPTCPVVAETKHFLLYSSGCKEQLRPSFLSLRPSLTGARL 360
Qy 361 VETIFLGSRRPMPGTERRLPRLPQRYQMRPLFLELIGNAQCPRYGLKTHCPLEAAVT 420
Db 361 VETIFLGSRRPMPGTERRLPRLPQRYQMRPLFLELIGNAQCPRYGLKTHCPLEAAVT 420
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Qy 481 RHNERRLRNTKRFISLQKNAKLSLQELTWKMSVRCAMLRSPGVGCPAPAEHRLREET 540
Db 481 RHNERRLRNTKRFISLQKNAKLSLQELTWKMSVRCAMLRSPGVGCPAPAEHRLREET 540
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Db 541 LAKTFLHMSVYVVELLRSPFYVETTFQCKNRLFFYAPSWSKLQSTGIRQHILKRYLRE 600
Qy 601 LSEAEVQKHEARFALLTSRLRFLPKPDGLRPIVNMVYVAGARTFRREKAEHLTSRYVA 660
Db 601 LSEAEVQKHEARFALLTSRLRFLPKPDGLRPIVNMVYVAGARTFRREKAEHLTSRYVA 660
Qy 661 LFSVLYNERARPPGLGASVGLDDIHRAMRTFVLRAADPPPELYFVAVDTGAYDTI 720
Db 661 LFSVLYNERARPPGLGASVGLDDIHRAMRTFVLRAADPPPELYFVAVDTGAYDTI 720
Qy 721 POBLTETVIASITKPONTYCVRRYAVYQKAAHGHVRAKAFKSHVSTLTDLPYKROFAHL 780
Db 721 POBLTETVIASITKPONTYCVRRYAVYQKAAHGHVRAKAFKSHVSTLTDLPYKROFAHL 780
Qy 781 QETSFLDVAVIEGSSSLNEASGLFVPLRPMCHAVRIRGKSYVOCQGIPOGSLISSL 840
Db 781 QETSFLDVAVIEGSSSLNEASGLFVPLRPMCHAVRIRGKSYVOCQGIPOGSLISSL 840
Qy 841 LCSIQYMDMNRKIFAGIRPDGLLRIVDDPLVTPHLTHAKTILRTLVREVPVGCVMNL 900
Db 841 LCSIQYMDMNRKIFAGIRPDGLLRIVDDPLVTPHLTHAKTILRTLVREVPVGCVMNL 900
Qy 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGILLDRTLLEVDSSYARTSIRASVTP 960
Db 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGILLDRTLLEVDSSYARTSIRASVTP 960
Qy 961 NRGKAGRNMRKIFGVLRLKCHSLFLDLQVNSIQVCTNIYKILLQAVRFAACVQLP 1020
Db 961 NRGKAGRNMRKIFGVLRLKCHSLFLDLQVNSIQVCTNIYKILLQAVRFAACVQLP 1020
Qy 1021 FHQGVNMPTEFLFVISTDASLCSILKAKAGMSLGAAGAPLSEAVQWMLCHQAFLL 1080
Db 1021 FHQGVNMPTEFLFVISTDASLCSILKAKAGMSLGAAGAPLSEAVQWMLCHQAFLL 1080
Qy 1081 KLTHRRVYVVLGSLRTAQOLSRKIPGTTLLLEAANPALPSPDKITLD 1132
Db 1081 KLTHRRVYVVLGSLRTAQOLSRKIPGTTLLLEAANPALPSPDKITLD 1132

RESULT 22
US-09-402-181B-611
Sequence 611, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Czech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aussenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 611:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1154 /note= "fusion protein composed of hTERT
OTHER INFORMATION: protein sequence, vector sequences, the
Myc epitope and His6 tag"
SEQUENCE DESCRIPTION: SEQ ID NO: 611:
US-09-402-181B-611

Query Match 99.8%; Score 5952; DB 4; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRLSLRSHYREVLPLATFVRLPQCRRLVQRGDPAPAFRLVAQCCLVCPW 60
DB 1 MPRAPRCRAVRLSLRSHYREVLPLATFVRLPQCRRLVQRGDPAPAFRLVAQCCLVCPW 60

QY 61 DARPPAPAFRCFVSLCKELVARVLQRLCERGAKNVLAFCFALLDGAAGPPEATTSVR 120
DB 61 DARPPAPAFRCFVSLCKELVARVLQRLCERGAKNVLAFCFALLDGAAGPPEATTSVR 120

QY 121 SYLNTVTDALRSGGAMGLLRRVGDVIVHLLARCALVLAAPSCAVOCBPPLYQLGA 180
DB 121 SYLNTVTDALRSGGAMGLLRRVGDVIVHLLARCALVLAAPSCAVOCBPPLYQLGA 180

QY 181 ATQAPRPPHAGSGRRRLGGERAMNHSVREAGVPLGLPAPGARRGGSASRSLPLKRRPR 240
DB 181 ATQAPRPPHAGSGRRRLGGERAMNHSVREAGVPLGLPAPGARRGGSASRSLPLKRRPR 240

QY 241 GAAPBEERTPVGGSWAHFPGTRGSDRGFCVSPAPAEATSLGALSGTRHSPVG 300
DB 241 GAAPBEERTPVGGSWAHFPGTRGSDRGFCVSPAPAEATSLGALSGTRHSPVG 300

QY 301 ROHHAAPSTSPRRPMDTCCPVYAEKHFLYSSGDKQLRPSFLSLSTRSLTGARL 360
DB 301 ROHHAAPSTSPRRPMDTCCPVYAEKHFLYSSGDKQLRPSFLSLSTRSLTGARL 360

QY 361 VETIFLGSRRPMGTRRLPLRQRYWQRPFLLELGNHACCPYVLKTHCPRAAVT 420
DB 361 VETIFLGSRRPMGTRRLPLRQRYWQRPFLLELGNHACCPYVLKTHCPRAAVT 420

QY 421 PAAGVACAREKPOGSVAAPBEEDTPRRRLVQLRQSSPWQVGFPAACIRLVPEGLMG 480
DB 421 PAAGVACAREKPOGSVAAPBEEDTPRRRLVQLRQSSPWQVGFPAACIRLVPEGLMG 480

QY 481 RHEHRRFLNTKFKFELGKHAKLLOELTWKMSVDCAWLRSPGVGCPAAEHRLREI 540
DB 481 RHEHRRFLNTKFKFELGKHAKLLOELTWKMSVDCAWLRSPGVGCPAAEHRLREI 540

QY 541 LAKEFLHMSVYVEILRSFYVETTFOKNLFYRPSVMSKIOSIGIRHKKVQURE 600
DB 541 LAKEFLHMSVYVEILRSFYVETTFOKNLFYRPSVMSKIOSIGIRHKKVQURE 600

QY 601 LSEAEVRQREARPAALLISRLRPIKPDGLRPIVMDYVVGARTRERERARLTSRYKA 660
DB 601 LSEAEVRQREARPAALLISRLRPIKPDGLRPIVMDYVVGARTRERERARLTSRYKA 660

QY 661 LPSVLNVEBARREGLGASVLGLDJIHRAMRTFVLRAODPPBELYFKVDVTGAYDTI 720
DB 661 LPSVLNVEBARREGLGASVLGLDJIHRAMRTFVLRAODPPBELYFKVDVTGAYDTI 720

QY 721 PODRLTEVIASTIKPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLOPQMCFVHL 780
DB 721 PODRLTEVIASTIKPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLOPQMCFVHL 780

QY 781 QETSPLRDAVLEOSSSLNEASSGLFDVFLRFMCHAVRIRKSYVQCGIPQGSILSTL 840
DB 781 QETSPLRDAVLEOSSSLNEASSGLFDVFLRFMCHAVRIRKSYVQCGIPQGSILSTL 840

QY 841 LQSLCYGDMENKLFAGIRRDGLLRVDFLLVTHLTHAKFTLTLVRGVEYGCYNL 900
DB 841 LQSLCYGDMENKLFAGIRRDGLLRVDFLLVTHLTHAKFTLTLVRGVEYGCYNL 900

QY 901 RKTUVNFPVEDALGTAFTVQMPAHGLFPMGCLLDTRTLEVOSSYSSYASTSRASVTF 960
DB 901 RKTUVNFPVEDALGTAFTVQMPAHGLFPMGCLLDTRTLEVOSSYSSYASTSRASVTF 960

QY 961 NRGFYAGRNRRKLFQVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYFFHACVQLP 1020
DB 961 NRGFYAGRNRRKLFQVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYFFHACVQLP 1020

QY 1021 FHQGVKNPTFFLRVISTDTSILCYSLKAKNAGMSLGAKGAPLPSEAVQWLCHQAFLL 1080
DB 1021 FHQGVKNPTFFLRVISTDTSILCYSLKAKNAGMSLGAKGAPLPSEAVQWLCHQAFLL 1080

QY 1081 KLTFRRTYVPLUGSLTAOTOLSRKLPCTTLTALBAANPALPSPFKTLLD 1132
DB 1081 KLTFRRTYVPLUGSLTAOTOLSRKLPCTTLTALBAANPALPSPFKTLLD 1132

RESULT 23
US-09-721-456-611
Sequence 611, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Mortin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/176.8
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 611:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
TYPE: amino acid

STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1154
 OTHER INFORMATION: /note= "fusion protein composed of hTERT
 protein sequence, vector sequences, the
 Myc epitope and His6 tag"
 SEQUENCE DESCRIPTION: SEQ ID NO: 611:
 US-09-721-456-611

Query Match 99.8%; Score 5952; DB 4; Length 1154;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAFCRAVRSLSRSHYREVLPATFVRSLGPGQWMLVORGDPAAFRALVAQCVCVPM 60
 Db 1 MPRAFCRAVRSLSRSHYREVLPATFVRSLGPGQWMLVORGDPAAFRALVAQCVCVPM 60
 QY 61 DARPPAPASFRQVSLKELVAVYLOLRCRGAKNTLAFGALLDQARGSPPAFTTSVR 120
 Db 61 DARPPAPASFRQVSLKELVAVYLOLRCRGAKNTLAFGALLDQARGSPPAFTTSVR 120
 QY 121 SYLPNTVTDALRGSGAGLLLRVGDVYLHLARCALFVLVAPSCAYQCGPPLVQLGA 180
 Db 121 SYLPNTVTDALRGSGAGLLLRVGDVYLHLARCALFVLVAPSCAYQCGPPLVQLGA 180
 QY 181 ATOARPPPHASGPPRRRLGCEBAMNHSVREAGVPLGLPAPARRGGASASRLPLPRPR 240
 Db 181 ATOARPPPHASGPPRRRLGCEBAMNHSVREAGVPLGLPAPARRGGASASRLPLPRPR 240
 QY 241 GAAPERTVYGQSGMAHPGRTGSPDRGCVVSPAPAEATSLGALSGTSHSPVY 300
 Db 241 GAAPERTVYGQSGMAHPGRTGSPDRGCVVSPAPAEATSLGALSGTSHSPVY 300
 QY 301 ROHHAGPSTSRPRPMDTCPPIVYATKFLYSSGDKQLRPSFLSSLRPSLTGARSL 360
 Db 301 ROHHAGPSTSRPRPMDTCPPIVYATKFLYSSGDKQLRPSFLSSLRPSLTGARSL 360
 QY 361 VERTFLGSRPMPGTPRRLPRLPQRYWQMBPLLELLGNHACCPYGLTKHPEPLAAAT 420
 Db 361 VERTFLGSRPMPGTPRRLPRLPQRYWQMBPLLELLGNHACCPYGLTKHPEPLAAAT 420
 QY 421 PAAGVCAKREKQGSVAPEEEDTDPRLYOLLRQSSPMQVYGFVBACTRLVPPGLMS 480
 Db 421 PAAGVCAKREKQGSVAPEEEDTDPRLYOLLRQSSPMQVYGFVBACTRLVPPGLMS 480
 QY 481 RHNERRLRNTKFKFISLGKIAKSLQELTWKMSVDCAMLRSPGVGCVAEHRIRBEI 540
 Db 481 RHNERRLRNTKFKFISLGKIAKSLQELTWKMSVDCAMLRSPGVGCVAEHRIRBEI 540
 QY 541 LAKFLHLMGVVYVELRSFFVYTETFQKNRLFEVYPSVMSKLOSIGIQHAKRYOLE 600
 Db 541 LAKFLHLMGVVYVELRSFFVYTETFQKNRLFEVYPSVMSKLOSIGIQHAKRYOLE 600
 QY 601 LSAEAVRQHRDEARPAITSLRPLPKPDGLRPIVNDYVVGATFRREKAEELTSRYVA 660
 Db 601 LSAEAVRQHRDEARPAITSLRPLPKPDGLRPIVNDYVVGATFRREKAEELTSRYVA 660
 QY 661 LFSVLANERARRPGLGASVLGLDDIRAWRTVLRADDPPELFFVAVDTGAYDTI 720
 Db 661 LFSVLANERARRPGLGASVLGLDDIRAWRTVLRADDPPELFFVAVDTGAYDTI 720
 QY 721 POGRLEVIASIIKQNTYCVRRYAVVQKAHGVKAFKFSHTLTDLPYKQCEVAHL 780
 Db 721 POGRLEVIASIIKQNTYCVRRYAVVQKAHGVKAFKFSHTLTDLPYKQCEVAHL 780
 QY 781 QETSPFLDAVYIEQSSINBASGLFDVFLRFMCHAVRIRGMSYVQCGQIPGGSILSTL 840
 Db 781 QETSPFLDAVYIEQSSINBASGLFDVFLRFMCHAVRIRGMSYVQCGQIPGGSILSTL 840
 QY 841 LCSLCYGDMEKLFAGIRBDGLLRVLVDLFLVPLTHAKTFLRLVGRVPEYGCVM 900

Db 841 LCSLCYGDMEKLFAGIRBDGLLRVLVDLFLVPLTHAKTFLRLVGRVPEYGCVM 900
 QY 901 RTIVNPFVEDEALAGTAFVQMPAHGLFPMCGLLDTRTEVQSDYSSYARTSIRASVTF 960
 Db 901 RTIVNPFVEDEALAGTAFVQMPAHGLFPMCGLLDTRTEVQSDYSSYARTSIRASVTF 960
 QY 961 NRGFAGKMRKILFGVRLKCHSLFIDLQVNSIQVCTNIYKILLLOAYRFFHACVQLP 1020
 Db 961 NRGFAGKMRKILFGVRLKCHSLFIDLQVNSIQVCTNIYKILLLOAYRFFHACVQLP 1020
 QY 1021 PHQGVKAPTFELRYISDTASLCYSILKAKNAGMSLGAAGAPLPSBAVOMLCHQAFIL 1080
 Db 1021 PHQGVKAPTFELRYISDTASLCYSILKAKNAGMSLGAAGAPLPSBAVOMLCHQAFIL 1080
 QY 1081 KLTRRRTVYVPLGSLRTAQTLSRKLPGTTLTALMAANPALPSDFKTIID 1132
 Db 1081 KLTRRRTVYVPLGSLRTAQTLSRKLPGTTLTALMAANPALPSDFKTIID 1132

RESULT 24
 US-08-974-549A-613
 ; Sequence 613, Application US/08974549A
 ; Patent No. 6166178
 ; GENERAL INFORMATION:
 ; APPLICANT: Cecch, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morlin, Gregg B.
 ; APPLICANT: Harley, Calvin B.
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 727
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974, 549A
 ; FILING DATE: 19-NOV-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724, 643
 ; FILING DATE: 01-OCT-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/844, 419
 ; FILING DATE: 18-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/851, 843
 ; FILING DATE: 06-MAY-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/854, 050
 ; FILING DATE: 09-MAY-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/911, 312
 ; FILING DATE: 14-AUG-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/912, 951
 ; FILING DATE: 14-AUG-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/915, 503

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FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1189
OTHER INFORMATION: /note="fusion protein composed of
OTHER INFORMATION: melittin signal sequence and full length
OTHER INFORMATION: h1rt protein
US-08-974-549a-613

Query Match          99.8%; Score 5952; DB 3; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPFCRAVRSLSLRHREYVPLATFYARLPGQCHLYQRDDPAFAFALVAQCVCVPM 60
DB 58 MRAPFCRAVRSLSLRHREYVPLATFYARLPGQCHLYQRDDPAFAFALVAQCVCVPM 117
QY 61 DARPPAASFRQVSCLEKELVARVLCRLCERGAKNVLAFFALDGAAGPPEATTTSVR 120
DB 118 DARPPAASFRQVSCLEKELVARVLCRLCERGAKNVLAFFALDGAAGPPEATTTSVR 177
QY 121 SYLENTVTDALRGSGAMGILLRRVGDVVLHLLARCAFLVAAPSCAYQVCGPPLYLQGA 180
DB 178 SYLENTVTDALRGSGAMGILLRRVGDVVLHLLARCAFLVAAPSCAYQVCGPPLYLQGA 237
QY 181 ATOQARPPHAGSGRRRLGGERAMNSVREAGVPLGLPAGARRGGSASRSLLPFRPRR 240
DB 238 ATOQARPPHAGSGRRRLGGERAMNSVREAGVPLGLPAGARRGGSASRSLLPFRPRR 297
QY 241 GAAPBERTPVQGSWAHPRTGSDRGFCVVSAPARPAEATSLGALSGTRHSHPSVG 300
DB 298 GAAPBERTPVQGSWAHPRTGSDRGFCVVSAPARPAEATSLGALSGTRHSHPSVG 357
QY 301 RQHHAGPSTSPRRPMDTCEPPVYAEFHFIYSGDKEQLRPSFLLSIRPSLTGARL 360
DB 358 RQHHAGPSTSPRRPMDTCEPPVYAEFHFIYSGDKEQLRPSFLLSIRPSLTGARL 417
QY 361 VETIFLGSRRPMWGTPLRLPLPORYQWRPLFELIGNHAQCPGVLLKTCPLRAAVT 420
DB 418 VETIFLGSRRPMWGTPLRLPLPORYQWRPLFELIGNHAQCPGVLLKTCPLRAAVT 477
QY 421 PAAGVCAAREKPOGSVAPEEDTDPRRLVQLRQSSPMQVYGFYACLCRLVPPGLMGS 480
DB 478 PAAGVCAAREKPOGSVAPEEDTDPRRLVQLRQSSPMQVYGFYACLCRLVPPGLMGS 537
QY 481 RHNRERFLNTKKFISLGHAHLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
DB 538 RHNRERFLNTKKFISLGHAHLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 597
QY 541 LAKFLHMLSVYVVELLSFFVYVETTFQKNLFFYRPSWSKLOSIGIRQHLKRVQURE 600
DB 598 LAKFLHMLSVYVVELLSFFVYVETTFQKNLFFYRPSWSKLOSIGIRQHLKRVQURE 657

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QY 601 LSEAEVQREARPAALITSLRFIPKPDGLRPIVMDYVVGATFRREKRAERTSRVKA 660
DB 658 LSEAEVQREARPAALITSLRFIPKPDGLRPIVMDYVVGATFRREKRAERTSRVKA 717
QY 661 LFSVLYNEARRRPGLIGASVTLGDDIHRAMRTVLRVADPPELFPKVDVTGAYDTI 720
DB 718 LFSVLYNEARRRPGLIGASVTLGDDIHRAMRTVLRVADPPELFPKVDVTGAYDTI 777
QY 721 PODRLTEVIAIIRKQNTYCVRRYAVYQKAAGHVKAFKSHVSTLTDLOPNRQFVAHL 780
DB 778 PODRLTEVIAIIRKQNTYCVRRYAVYQKAAGHVKAFKSHVSTLTDLOPNRQFVAHL 837
QY 781 QETSPLRDVAVITFOSSINASSGLFDVFLRFMCHAVNIRGSIYQCCGIPQGSITSLT 840
DB 838 QETSPLRDVAVITFOSSINASSGLFDVFLRFMCHAVNIRGSIYQCCGIPQGSITSLT 897
QY 841 LGSICYGDMENKLPAGIRSDGLRLRVDDFLVTPHILAKTFLRLTVAGVEYGCVNL 900
DB 898 LGSICYGDMENKLPAGIRSDGLRLRVDDFLVTPHILAKTFLRLTVAGVEYGCVNL 957
QY 901 RKTIVANFVEDELGGTAFVQMAHGLFPWCGILLDTRTLLEVQSDYSYARISIRSLTF 960
DB 958 RKTIVANFVEDELGGTAFVQMAHGLFPWCGILLDTRTLLEVQSDYSYARISIRSLTF 1017
QY 961 NRGFKGRNRRKLPGLRLKCHSLFLDLQVNSLOTVCNIIYKILLQAYRPHACVLOLP 1020
DB 1018 NRGFKGRNRRKLPGLRLKCHSLFLDLQVNSLOTVCNIIYKILLQAYRPHACVLOLP 1077
QY 1021 FHOQWKNPFLPLRVISDTASLCYSILKAKNAGMSIGAKGAAPLPSBAVOMLCHOAFIL 1080
DB 1078 FHOQWKNPFLPLRVISDTASLCYSILKAKNAGMSIGAKGAAPLPSBAVOMLCHOAFIL 1137
QY 1081 KLTRHRVTYVPLIGSLRTQOTLSRKLPGTTLTALSAANPALPSDFKITLD 1132
DB 1138 KLTRHRVTYVPLIGSLRTQOTLSRKLPGTTLTALSAANPALPSDFKITLD 1189

RESULT 25
US-08-912-951-325
Sequence 325, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-325

Query Match      99.8%; Score 5952; DB 4; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAFRCAVRSLLRSHRYEVLPLATFVRRLPGQGMRLVORGDPAPFALVACLVCPM 60
DB 58 MPRAFRCAVRSLLRSHRYEVLPLATFVRRLPGQGMRLVORGDPAPFALVACLVCPM 117

QY 61 DAPPPAPSPFRQVSCIKELVAVYLQRLCERGANVLAFCFALLDGRGPPPAFTTSVR 120
DB 118 DAPPPAPSPFRQVSCIKELVAVYLQRLCERGANVLAFCFALLDGRGPPPAFTTSVR 177

QY 121 SYLPTVTDLRSGAGWGLLRVGDVIVHLLARCLFTLVAPSCYVCGEPYQLQ 180
DB 178 SYLPTVTDLRSGAGWGLLRVGDVIVHLLARCLFTLVAPSCYVCGEPYQLQ 237

QY 181 ATOARPPPHASGPRRLGGERAMNHSYREAGVPLGLPAPGARRGGSASRLPLPKRPR 240
DB 238 ATOARPPPHASGPRRLGGERAMNHSYREAGVPLGLPAPGARRGGSASRLPLPKRPR 297

QY 241 GAAPERTPTVGGQSMHAPGRTGPRSDRGFCVSPAPAEALSLGALSGTHSPSVG 300
DB 298 GAAPERTPTVGGQSMHAPGRTGPRSDRGFCVSPAPAEALSLGALSGTHSPSVG 357

QY 301 ROHAGSPSTSRPMPDTCPPRYAETKHFIVSSGDKQLRPSFLSLSRPLTGARRL 360
DB 358 ROHAGSPSTSRPMPDTCPPRYAETKHFIVSSGDKQLRPSFLSLSRPLTGARRL 417

QY 361 VETIFLGSRRPMPGTPRLPLPRLFORVQMRPLFLIELIGNFAQCPRYVLLKTHCPPLAAVT 420
DB 418 VETIFLGSRRPMPGTPRLPLPRLFORVQMRPLFLIELIGNFAQCPRYVLLKTHCPPLAAVT 477

QY 421 PAVGVCAKREPOGQVAPEEDDPRLVOLLROHSSPMOVYGVPRACLRPLPGLMGS 480
DB 478 PAVGVCAKREPOGQVAPEEDDPRLVOLLROHSSPMOVYGVPRACLRPLPGLMGS 537

QY 481 RHNERRLRNTKPSISGKAHKLQELTWKMSVRCAMLRSPGVCVPAASHRLREEL 540
DB 538 RHNERRLRNTKPSISGKAHKLQELTWKMSVRCAMLRSPGVCVPAASHRLREEL 597

QY 541 LAKFLHMLMSVYVELLSFFVYVETTFQKNRLFFYRPSVMSKLSQSIGIRHKLKVQLRE 600

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DB 598 LAKFLHMLMSVYVELLSFFVYVETTFQKNRLFFYRPSVMSKLSQSIGIRHKLKVQLRE 657
QY 601 LSEAEVRQHRERAPALTSRLRFIPKPGDLPIYVMQDVYVARTPRERKREPLTSRKA 660
DB 658 LSEAEVRQHRERAPALTSRLRFIPKPGDLPIYVMQDVYVARTPRERKREPLTSRKA 717
QY 661 LFSVLNYSRARRPGJLGASVGLDIDHRAWTFVLVRAADPPPELYFVKYDVTGAYDTI 720
DB 718 LFSVLNYSRARRPGJLGASVGLDIDHRAWTFVLVRAADPPPELYFVKYDVTGAYDTI 777
QY 721 PODRLTEVIASIKQNTYCYRRYAVVOKAAGHVRKAFKHVSTLTDLOPYMQFVHL 780
DB 778 PODRLTEVIASIKQNTYCYRRYAVVOKAAGHVRKAFKHVSTLTDLOPYMQFVHL 837
QY 781 CETSPLRDAVYIEQSSSINEASSGLFDVFLRFMCHHAVRIRKSYVCCGIPQGSILSTL 840
DB 838 CETSPLRDAVYIEQSSSINEASSGLFDVFLRFMCHHAVRIRKSYVCCGIPQGSILSTL 897
QY 841 LCSLCYGMENKLPFGIRRDGLLRVDDFLVTPHLLTHAKTFLRTLVRYGVEYGVNVL 900
DB 898 LCSLCYGMENKLPFGIRRDGLLRVDDFLVTPHLLTHAKTFLRTLVRYGVEYGVNVL 957
QY 901 RKTIVNFPVEDBALDGTAFVQMPAHGLFPMCGLLDTRTLVQSDYSYARTSTRASVTF 960
DB 958 RKTIVNFPVEDBALDGTAFVQMPAHGLFPMCGLLDTRTLVQSDYSYARTSTRASVTF 1017
QY 961 NEGFAGSNMRKLFGLVRLKCHSLFDLDQVNSIQVCTNYYKILLQAFHACVQLP 1020
DB 1018 NEGFAGSNMRKLFGLVRLKCHSLFDLDQVNSIQVCTNYYKILLQAFHACVQLP 1077
QY 1021 FHOQVWKXPTFFLRITSDTASCYSILKAKNAGMSLGKGAAPLPSAVQMLCHQARLL 1080
DB 1078 FHOQVWKXPTFFLRITSDTASCYSILKAKNAGMSLGKGAAPLPSAVQMLCHQARLL 1137
QY 1081 KLTRHRYVYVPLGLSLRTAQQLSRKLPGLTLTLEAANPALPSDFETIIL 1132
DB 1138 KLTRHRYVYVPLGLSLRTAQQLSRKLPGLTLTLEAANPALPSDFETIIL 1189

RESULT 26
US-09-402-181B-613
; Sequence 613, Application US/09402181B
; Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Udochlm
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419

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FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 23-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenius, Scott J.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1189
OTHER INFORMATION: /note= "fusion protein composed of
melittin signal sequence and full length
hTERT protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-09-402-181B-613
Query Match 99.8%; Score 5952; DB 4; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRAPRCRAVRSLSHREVLPLATFVRRLGPGMRVLVGRDPAAPALVAQCIVCPM 60
DB 58 MPAPRCRAVRSLSHREVLPLATFVRRLGPGMRVLVGRDPAAPALVAQCIVCPM 117
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QY 121 STLENTVTALGSGAMGILLRRVGDVYLHLLACALFVVAECAYQVCPPLYQGA 180
DB 178 STLENTVTALGSGAMGILLRRVGDVYLHLLACALFVVAECAYQVCPPLYQGA 237
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DB 238 ATQARPPHAGSPRRRLGGERAMNHSVREAGVPLGLPAGARRRGSASRSLPLPKRPR 297
QY 241 GAAPERTIPVQGSNAHPGRTGSPDRGFCVVASPARPAEATSLLEGALSGTRHSHSVG 300
DB 298 GAAPERTIPVQGSNAHPGRTGSPDRGFCVVASPARPAEATSLLEGALSGTRHSHSVG 357
QY 301 RQHHAGPSTSPRRWDTCPPVYAETKHFILYSSGDKKOLRPSFLSLSLTSLGARRL 360
DB 358 RQHHAGPSTSPRRWDTCPPVYAETKHFILYSSGDKKOLRPSFLSLSLTSLGARRL 417
QY 361 VETIFLGSRRPMWGTGPRRLRPLRQRYWQNRPLFLELLGNHACPFYVLLKTHCPRAAVT 420
DB 418 VETIFLGSRRPMWGTGPRRLRPLRQRYWQNRPLFLELLGNHACPFYVLLKTHCPRAAVT 477
QY 421 PPAAGVCAARKPGSVAAPEEEDTDPRRLVQLLRQSSPMQVYGFRAALRLRVPPEGLMS 480
DB 478 PPAAGVCAARKPGSVAAPEEEDTDPRRLVQLLRQSSPMQVYGFRAALRLRVPPEGLMS 537

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QY 481 RHNERRLRNTKTKFISIGKAKISLOELTMKMSVRDCAELRSPGVGVPAAEHRLREI 540
DB 538 RHNERRLRNTKTKFISIGKAKISLOELTMKMSVRDCAELRSPGVGVPAAEHRLREI 597
QY 541 LAKFLHMLSVVYVELRSEFFVTEFTFOKNRLFFRPSWSTLQSIGIRHLKRYOLHE 600
DB 598 LAKFLHMLSVVYVELRSEFFVTEFTFOKNRLFFRPSWSTLQSIGIRHLKRYOLHE 657
QY 601 LSEAEVQHEARPAALITSLRFLFKPDGIRPLVNMDDYVGAATFRERGAELTSRYVA 660
DB 658 LSEAEVQHEARPAALITSLRFLFKPDGIRPLVNMDDYVGAATFRERGAELTSRYVA 717
QY 661 LFSVLNTERARRPGLLGASVLTGLDDIHRAMRTVLRAADPEPELYFKVDVTGAYDTI 720
DB 718 LFSVLNTERARRPGLLGASVLTGLDDIHRAMRTVLRAADPEPELYFKVDVTGAYDTI 777
QY 721 PDRLTEVIASIIKPPONTYCVRRYAVVQKAHGVAKAFKSHVSTLTDIQPMRCVANH 780
DB 778 PDRLTEVIASIIKPPONTYCVRRYAVVQKAHGVAKAFKSHVSTLTDIQPMRCVANH 837
QY 781 QETSPLDAAVIVQSSSLNASSGLPDLFRFVCHAVIRGKSYQCCGIPQGSILSTL 840
DB 838 QETSPLDAAVIVQSSSLNASSGLPDLFRFVCHAVIRGKSYQCCGIPQGSILSTL 897
QY 841 LGSICYDMMENKLPAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRLVGVPEYGCVANL 900
DB 898 LGSICYDMMENKLPAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRLVGVPEYGCVANL 957
QY 901 RKTVANPVEDEALGGTAAPQWPAHGLFPMCGILLDTRTLEVQSDSSYARTSIRASYNF 960
DB 958 RKTVANPVEDEALGGTAAPQWPAHGLFPMCGILLDTRTLEVQSDSSYARTSIRASYNF 1017
QY 961 NRGFKAGRRNRRLFGVLRKCHSLFLDLQVNSLQTCVNTNIXILLQAYRPAVCLQUP 1020
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DB 1078 PHQQWKNPFFELRVISDTNALSICSTILKAKNAGMSIGANGAGPLFSEAVQMLCHQAFLL 1137
QY 1081 KLTRHRVTYVPLGSLRTAQOTLSRLPGTTTLALAAANPALSPDFKILL 1132
DB 1138 KLTRHRVTYVPLGSLRTAQOTLSRLPGTTTLALAAANPALSPDFKILL 1189

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RESULT 27
 US-09-721-456-613
 Sequence 613, Application US/09721456
 Patent No. 6617110
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESSES:
 ADDRESSER: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

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      APPLICATION NUMBER: US/09/721,456
      FILING DATE: 22-Nov. 6617110-2000
      CLASSIFICATION: <unknown>
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/08/974,549A
      FILING DATE: 19-NOV-1997
      APPLICATION NUMBER: US 08/724,643
      FILING DATE: 01-OCT-1996
      APPLICATION NUMBER: US 08/844,419
      FILING DATE: 18-APR-1997
      APPLICATION NUMBER: US 08/846,017
      FILING DATE: 25-APR-1997
      APPLICATION NUMBER: US 08/851,843
      FILING DATE: 06-MAY-1997
      APPLICATION NUMBER: US 08/854,050
      FILING DATE: 09-MAY-1997
      APPLICATION NUMBER: US 08/911,312
      FILING DATE: 14-AUG-1997
      APPLICATION NUMBER: US 08/912,951
      FILING DATE: 14-AUG-1997
      APPLICATION NUMBER: US 08/915,503
      FILING DATE: 14-AUG-1997
      APPLICATION NUMBER: WO PCT/US97/17618
      FILING DATE: 01-OCT-1997
      APPLICATION NUMBER: WO PCT/US97/17885
      FILING DATE: 01-OCT-1997
      ATTORNEY/AGENT INFORMATION:
      NAME: Apple, Randolph Ted
      REGISTRATION NUMBER: 36,429
      REFERENCE/DOCKET NUMBER: 015389-002610US
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 576-0200
      TELEFAX: (415) 576-0300
      INFORMATION FOR SEQ ID NO: 613:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 1189 amino acids
      TYPE: amino acid
      STRANDEDNESS: <unknown>
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      FEATURE:
      NAME/KEY: Protein
      LOCATION: 1..1189
      OTHER INFORMATION: /note="fusion protein composed of
      telitxin signal sequence and full length
      hprt protein"
      SEQUENCE DESCRIPTION: SEQ ID NO: 613:
      US-09-721-456-613
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      Best Local Similarity 99.8%; Pred. No. 0;
      Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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      DB      178 SYLPNTVTDALRSGAMGILLIRVGDVVLVHLIARCALFVLVAPSCAYQVCGPPIYQLGA 237
      QY      181 ATGAPPPHAGSGRRRLGCEBAMNHAVREGVPLIGLPAPGARRGGSASRLPLPRPRR 240
      DB      238 ATGAPPPHAGSGRRRLGCEBAMNHAVREGVPLIGLPAPGARRGGSASRLPLPRPRR 297
      QY      241 GAAPPEPRTVGQGSVNAHPGRTGSPDRGFCVSPAPAPAEATSLGALSGTRHSHPSVG 300
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      QY      301 ROHNAAPSTSRPPRPMDTPCGPVYAETKHFLLYSSGDKEQLRPSLLSLRSLTGARL 360
      DB      356 ROHNAAPSTSRPPRPMDTPCGPVYAETKHFLLYSSGDKEQLRPSLLSLRSLTGARL 417
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      DB      478 PAAGVCAEKPQGSVAAPBEEDTPRRRLVOLLROHSPWQYGFAPRACLRRLVPPGLWGS 537
      QY      481 RHNERFLRNTKFTSLGKHAQLSIQELTWKMSVDCAMLRSPQVGCVPAAEHRLREI 540
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      DB      598 LAKELHMLMSVYVVELASFPYVETTFQKRLPFYRSVMSKLSIGIRHLKRYQVIRE 657
      QY      601 LSEAEVRQHRERAPALTSRLRFLPKPDGLRPVMMDYVGARTFRERKARERLTSRYKA 660
      DB      658 LSEAEVRQHRERAPALTSRLRFLPKPDGLRPVMMDYVGARTFRERKARERLTSRYKA 717
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      DB      838 QETSPLRDAVVIQSSSINERASSGLFDVFLRFMCHAVRIRGKSYVQCGIPQGSII STL 897
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      QY      961 NRGFKAGNNMRKLPGVRLKCHSLFDLDQVNSIQVCTNITKILLQAVRFHACVQLP 1020
      DB      1018 NRGFKAGNNMRKLPGVRLKCHSLFDLDQVNSIQVCTNITKILLQAVRFHACVQLP 1077
      QY      1021 FHQVWKMPDTFFLRITSDTASLCYSILKAKNAGSLGAKGAGLPSEAVQMLCHQAFLL 1080
      DB      1078 FHQVWKMPDTFFLRITSDTASLCYSILKAKNAGSLGAKGAGLPSEAVQMLCHQAFLL 1137
      QY      1081 KLTRRRVTYVPLGSLRTAQQLSRKLPGLTTLALEAANPALPSDEKTIID 1132
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      RESULT 28
      US-08-974-549A-612
      / Sequence 612; Application US/08974549A
      / Patent No. 6166178
      / GENERAL INFORMATION:
      / APPLICANT: Cech, Thomas R.
      / APPLICANT: Lininger, Joachim
      / APPLICANT: Nakamura, Toru
      / APPLICANT: Chapman, Karen B.
      / APPLICANT: Morley, Gregg B.
      / APPLICANT: Harley, Calvin B.
      / APPLICANT: Andrews, William H.
      / TITLE OF INVENTION: Human Telomerase Catalytic Subunit
      / NUMBER OF SEQUENCES: 727
      / CORRESPONDENCE ADDRESS:
      / ADDRESSEE: Townsend and Townsend and Crew LLP
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STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 612:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1200 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1200
 OTHER INFORMATION: /note="fusion protein composed of His6
 and Anti-Xpress tags, enterokinase
 OTHER INFORMATION: cleavage site and full length mrt
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 US-08-974-549A-612

Query Match 99.8%; Score 5952; DB 3; Length 1200;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1100; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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RESULT 29
 US-08-912-951-324
 Sequence 324, Application US/08912951
 Patent No. 6475789
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Hartley, Calvin
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/912,951
 FILING DATE: 14-AUG-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ. ID NO.: 324:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1200 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-912-951-324

Query Match 99.8%; Score 5952; DB 4; Length 1200;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY	601	LSEAEVQRHARAPALLTSRLRPIKPDGLRPYNNMDYVGARFRREKRAERLTSRYKA	660
DB	669	LSEAEVQRHARAPALLTSRLRPIKPDGLRPYNNMDYVGARFRREKRAERLTSRYKA	728
QY	661	LFSVLYNRYARAPGLIGASVGLDDIHRAMRTFYLRADQPPLELFVKYDVGADYTI	720
DB	729	LFSVLYNRYARAPGLIGASVGLDDIHRAMRTFYLRADQPPLELFVKYDVGADYTI	788
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DB	789	PODRLTEVIASIIKPNQTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMQFAHL	848
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DB	849	QETSRLRAVYIEOSSINENASGLFVFLRPMCHAVRIRGKSYVCCGIPGSSIIISTL	908
QY	841	LCSLCYGMENKTLFAGIRRDGILLRLVDDFLVTPHLLTHAKTFLRTLVGPEYGVNLT	900
DB	909	LCSLCYGMENKTLFAGIRRDGILLRLVDDFLVTPHLLTHAKTFLRTLVGPEYGVNLT	968
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DB	969	RKTYVNFVDEDEALGTAFFVMPAHGFPWCGILLDTRTLEVOGDYSSYARTSIRASTF	1028
QY	961	NRGEFAGNMRKLFVYLRLKCHSLFLDLOVNSLOTVCTNLYKILLQAYEFHACVQLP	1020
DB	1029	NRGEFAGNMRKLFVYLRLKCHSLFLDLOVNSLOTVCTNLYKILLQAYEFHACVQLP	1088
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QY	1081	KLTRHRYVYVLLGSLRTAQTOISRKLPGLTTLTLEAANPALPSDFKTIJD	1132

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RESULT 30
US-09-402-181B-612
Sequence 612, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
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APPLICATION NUMBER: US 08/854,050
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APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenius, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 612:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1200
OTHER INFORMATION: /note= "fusion protein composed of His6
and Anti-Xpress tags, enterokinase
cleavage site and full length hTERT

SEQUENCE DESCRIPTION: SEQ ID NO: 612:
US-09-402-181B-612
Protein
Query Match 99.8%; Score 5952; DB 4; Length 1200;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSILSRSHREVLPLATFVRRLPGQGRVLRQDPAAPRALVAQCLVCPW 60
Db MPRAPRCRAVRSILSRSHREVLPLATFVRRLPGQGRVLRQDPAAPRALVAQCLVCPW 128
QY 61 DARPAPAPSPFQVSGCLKEVLARVYLQRLCERGAQKVLAFGAPALLDQARGPEAFTSVR 120
Db DARPAPAPSPFQVSGCLKEVLARVYLQRLCERGAQKVLAFGAPALLDQARGPEAFTSVR 188
QY 129 DARPAPAPSPFQVSGCLKEVLARVYLQRLCERGAQKVLAFGAPALLDQARGPEAFTSVR 188
Db 121 SYLPTVTDLNRSGAMGILLRVDVYLHLLARCALFVLVAPSCAYQVCPPIYQGA 180
QY 189 SYLPTVTDLNRSGAMGILLRVDVYLHLLARCALFVLVAPSCAYQVCPPIYQGA 248
Db 181 ATQARPPHAPSGRRRLGGERAMNSVVRAGVPLGAPGARRGSGASRSILPLRPRR 240
QY 249 ATQARPPHAPSGRRRLGGERAMNSVVRAGVPLGAPGARRGSGASRSILPLRPRR 308
Db 241 GAAPBERTPVQGGSWAHBGRTRGSDRCFCVSPAPRAEATSLGALSGTRHSPVG 300
QY 309 GAAPBERTPVQGGSWAHBGRTRGSDRCFCVSPAPRAEATSLGALSGTRHSPVG 368
Db 301 RQHNAEPSTSRPPRPWDTPCPPVYAEKHFYISGDKQQLRPSFLSLRSLTGARL 360
QY 369 RQHNAEPSTSRPPRPWDTPCPPVYAEKHFYISGDKQQLRPSFLSLRSLTGARL 428
Db 361 VETIFGSRPMMGTRRLPLRLPORWQMRPLFLELGNHACCPGVLLKTHCPRAAVT 420
QY 429 VETIFGSRPMMGTRRLPLRLPORWQMRPLFLELGNHACCPGVLLKTHCPRAAVT 488
Db 421 PAAGVAREKPGQSVAPAEEDTDPRLVQLIRQSSPMQVGYFVACLRILVPPGLWS 480
QY 489 PAAGVAREKPGQSVAPAEEDTDPRLVQLIRQSSPMQVGYFVACLRILVPPGLWS 548
Db 481 RHNERELNKTKEFISLGHAKLSLOELTWKXSVRDCALRRSPGVCPALAEHRLREBI 540
QY 549 RHNERELNKTKEFISLGHAKLSLOELTWKXSVRDCALRRSPGVCPALAEHRLREBI 608
Db 541 LAKFLHMSVYVVELLRSPFYVTEETFOKNRLFYRPSWMSKLSIGIRQLKRVQLRE 600
QY 609 LAKFLHMSVYVVELLRSPFYVTEETFOKNRLFYRPSWMSKLSIGIRQLKRVQLRE 668
Db 601 LSAEVRQHRERAPALTLRLRFIPKPDGLRPIVMNDVVGARTRRERKARLISRYKA 660
QY 669 LSAEVRQHRERAPALTLRLRFIPKPDGLRPIVMNDVVGARTRRERKARLISRYKA 728
Db 661 LPSVLNVERARPPGLLGASVGLGDDIHRAMRTFVLRAQDPPPELYFVKVDVTGAYDTI 720
QY 729 LPSVLNVERARPPGLLGASVGLGDDIHRAMRTFVLRAQDPPPELYFVKVDVTGAYDTI 788
Db 721 PQRRLTEVIASIIKPNNTYCVRRYAVVOGAAGHRAKASHVSTLTDQPMRQFVAL 780
QY 789 PQRRLTEVIASIIKPNNTYCVRRYAVVOGAAGHRAKASHVSTLTDQPMRQFVAL 848
Db 781 QETSPLRDVAVIEQSSLINEASGLFDVFLRFMCHAAVIRKSYQCCGIIQGSILSTL 840
QY 849 QETSPLRDVAVIEQSSLINEASGLFDVFLRFMCHAAVIRKSYQCCGIIQGSILSTL 908
Db 841 LGSILCYGDMENKLPAGIRSDGLLRVLVDLFLVPHLTHAKTFLRTLVGVEPYGVVNL 900
QY 909 LGSILCYGDMENKLPAGIRSDGLLRVLVDLFLVPHLTHAKTFLRTLVGVEPYGVVNL 968
Db 901 RKTVMNPEVEDELGGTAFAVOMPAHGLTFMCGILLDTRLTEVQSDVSSYARISIRASVTF 960
QY 969 RKTVMNPEVEDELGGTAFAVOMPAHGLTFMCGILLDTRLTEVQSDVSSYARISIRASVTF 1028
Db 961 NRGFKAGRMWRKLPGLVRLKCHSLFLDQVNSLQTVCTNIYKILLQAYRFAVCLQLP 1020

DB 1029 NRPFKGRNRRLFGVLRKCHSLFDLDQVNSLQVCTNIVYKILLQAVRFACVLCIP 1088
QY 1021 FHQVWKNPTFFLRVSDTSLCYSLIKKAGMSIGAKGAGPLPSEAVOMLCHOAFIL 1080
DB 1089 FHQVWKNPTFFLRVSDTSLCYSLIKKAGMSIGAKGAGPLPSEAVOMLCHOAFIL 1148
QY 1081 KLTRHRYTVPLIGSLRTAQTOUSRLPGTTLTALBAANPALPSDFKTLID 1132
DB 1149 KLTRHRYTVPLIGSLRTAQTOUSRLPGTTLTALBAANPALPSDFKTLID 1200

RESULT 31
US-09-721-456-612
Sequence 612, Application US/09721456
Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov. 66/7110-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 612:

SEQUENCE CHARACTERISTICS:
LENGTH: 1200 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURES:
NAME/KEY: Protein
LOCATION: 1..1200
OTHER INFORMATION: /note="fusion protein composed of His6
and Anti-Xpress tags, enterokinase
cleavage site and full length hTERT
protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 612:
US-09-721-456-612

Query Match 99.8%; Score 5952; DB 4; Length 1200;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLIRSHYREVLPLATFVRLIGPGSMRLVQGDPAFPAVAQCVCVPM 60
DB 69 MPAPRCRAVSLIRSHYREVLPLATFVRLIGPGSMRLVQGDPAFPAVAQCVCVPM 128
QY 61 DARPAPAPSPROYSCLEKEIVARVLCRCERGANVLAFGPALLDGAAGGPEAFITSVR 120
DB 129 DARPAPAPSPROYSCLEKEIVARVLCRCERGANVLAFGPALLDGAAGGPEAFITSVR 188
QY 121 SYLPRTVTDALRGSGAWGLLRVGGDVLVHLARCALFVLAPSCAYOVQGPRLYOLGA 180
DB 189 SYLPRTVTDALRGSGAWGLLRVGGDVLVHLARCALFVLAPSCAYOVQGPRLYOLGA 248
QY 181 ATOARPPPHAGGPRRLUCERAMNHSHREAGVPLGLPAPGARREGGSASRLPLPKPRR 240
DB 249 ATOARPPPHAGGPRRLUCERAMNHSHREAGVPLGLPAPGARREGGSASRLPLPKPRR 308
QY 241 GAPEPEPTVPGQSMWHPGRTGSPDRCFCVSPAPPAEATLSEALSGTRSHSVG 300
DB 309 GAPEPEPTVPGQSMWHPGRTGSPDRCFCVSPAPPAEATLSEALSGTRSHSVG 368
QY 301 ROHAGPSTSPRPMDTPCPVYAEIKHPLYSQDKEQLRPSFLISSRLPSTGARRL 360
DB 369 ROHAGPSTSPRPMDTPCPVYAEIKHPLYSQDKEQLRPSFLISSRLPSTGARRL 428
QY 361 VETIFLIGSRPMPGTPRRLPLPORVOMRPLFELIGNHAQCYGLVLTCHCLRAVY 420
DB 429 VETIFLIGSRPMPGTPRRLPLPORVOMRPLFELIGNHAQCYGLVLTCHCLRAVY 488
QY 421 PAAGVCAEKQGVAAPEEEDTDPRLVOLLRSHSPWCYGVFVRACLRVPGLMG 480
DB 489 PAAGVCAEKQGVAAPEEEDTDPRLVOLLRSHSPWCYGVFVRACLRVPGLMG 548
QY 481 RHNRRLPLRNTKRTISGKAKLSLOELTWKMSRDCAMLRSGVCCVPAERLRLTEE 540
DB 549 RHNRRLPLRNTKRTISGKAKLSLOELTWKMSRDCAMLRSGVCCVPAERLRLTEE 608
QY 541 LAKELHWMISYVVELLRSFFVYETTFQKNRLFFPSPYSKLSQSIGIRHLRVLRE 600
DB 609 LAKELHWMISYVVELLRSFFVYETTFQKNRLFFPSPYSKLSQSIGIRHLRVLRE 668
QY 601 LSEAEVROHREARAPALLTSRLRFLPKPDGLRPYVNMVYVGARFFREKAERLTSVKA 660
DB 669 LSEAEVROHREARAPALLTSRLRFLPKPDGLRPYVNMVYVGARFFREKAERLTSVKA 728
QY 661 LFSVLYNERARPPGLGASVGLGDIHRAWTFELRAADPPEELFVKVDVGAADTI 720
DB 729 LFSVLYNERARPPGLGASVGLGDIHRAWTFELRAADPPEELFVKVDVGAADTI 788
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DB 789 PQRRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRAKFSHVSUTLTDLPYMQFYAHL 848
QY 781 QETSPRLDAVVIQSSSLNEASSGLPDVFLRFMCHNAVRLIRGKSYVQCGGIPGSSISTL 840

DB 849 CETSPLRAVYIEGSSLINEASSGIEFLEFPMCHHARNGKSYVCCQGIPOCSILSTL 908
DB 841 LCSLCYGMENKLEFAGIRRDGLLRVYDFLLVTPHLLTHAFTPLRLVRGVPEYCVNL 900
DB 909 LCSLCYGMENKLEFAGIRRDGLLRVYDFLLVTPHLLTHAFTPLRLVRGVPEYCVNL 968
DB 901 KRTVNFVEDEBALGCTAFVQMPAHGLEPFCGCLLDPTLTLEVOQDSSYASTSRASVTF 960
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DB 961 NRGFGAGRMREKLEFGVRLKCHSLFLDLQVNSLQVCTNIYKILLQAYRFLACVQLP 1020
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DB 1149 KLTRHRYVYVPLGSLRTAQQLSRKLEPGLTLLLEAANPALSPDFETILD 1200

RESULT 32
US-08-974-549A-600
Sequence 600, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 600:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1285
OTHER INFORMATION:
OTHER INFORMATION: chloreodoxin moiety and full length hTrrn
US-08-974-549A-600

Query Match 99.8%; Score 5952; DB 3; Length 1285;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 MPAPRCRAVRSILRSHREYVPLATFVRRLCPQGRRLVQRDDPAAFRLVACVQVW 60
DB 154 MPAPRCRAVRSILRSHREYVPLATFVRRLCPQGRRLVQRDDPAAFRLVACVQVW 213
DB 61 DARPPAAPSFRVSCLEKELVARVLQRLCERAKAVLAFGALLDGAARGSPPEAFTTSVR 120
DB 214 DARPPAAPSFRVSCLEKELVARVLQRLCERAKAVLAFGALLDGAARGSPPEAFTTSVR 273
DB 121 SYLNTVTALRSGAWGLLRVGGDVLVHLARCALFVLAFCAYVCCPPLYQLGA 180
DB 274 SYLNTVTALRSGAWGLLRVGGDVLVHLARCALFVLAFCAYVCCPPLYQLGA 333
DB 181 ATQARPEPHASGRRRLGGERAMNHSVRAGVPLGAPGARRGGSASRLPLPKRPR 240
DB 334 ATQARPEPHASGRRRLGGERAMNHSVRAGVPLGAPGARRGGSASRLPLPKRPR 393
DB 241 GAAPPERPTPVGGSWAHFGRTRGSDRGFCVYSPAPPAEATSLGALSTRHSHPSVG 300
DB 394 GAAPPERPTPVGGSWAHFGRTRGSDRGFCVYSPAPPAEATSLGALSTRHSHPSVG 453
DB 301 RQHHAGPSTSRPRRWDTPCPVVAETGHPLYSSGDKQLPSFLSLSLRSLGARRL 360
DB 454 RQHHAGPSTSRPRRWDTPCPVVAETGHPLYSSGDKQLPSFLSLSLRSLGARRL 513
DB 361 VETIFLGSRRPMWGTTPRLPLRQRYWQMRPLFELILGNHAOCPPVLLKTHCPRAAVT 420
DB 514 VETIFLGSRRPMWGTTPRLPLRQRYWQMRPLFELILGNHAOCPPVLLKTHCPRAAVT 573
DB 421 PAAGVCAREKPGSVAAPEEDTDPRRLVQLRQSSPMQVYGFTRACLRRLVPPRLWS 480
DB 574 PAAGVCAREKPGSVAAPEEDTDPRRLVQLRQSSPMQVYGFTRACLRRLVPPRLWS 633
DB 481 RHNERRLRNTKFKISLGKAKLSLDELTKWSVRDCAALRRSPGVGCVPAAEHRLREBI 540
DB 634 RHNERRLRNTKFKISLGKAKLSLDELTKWSVRDCAALRRSPGVGCVPAAEHRLREBI 693

QY 541 LAKELHLMGAVVVELLSFFVYTTTFOQNRLEFFRPSVWSKLSIGIRHOLKRYOLRE 600
 Db 694 LAKELHLMGAVVVELLSFFVYTTTFOQNRLEFFRPSVWSKLSIGIRHOLKRYOLRE 753
 QY 601 LSEAEVQHRREARPAALITSLRPLPKPDGLRPVNMDDYVGAATFRREKAEELISRVKA 660
 Db 754 LSEAEVQHRREARPAALITSLRPLPKPDGLRPVNMDDYVGAATFRREKAEELISRVKA 813
 QY 661 LFSVLYNERARRPGLIGASVGLGDDIHRAMRTVLRADPPPELYFVAVDTGAYDIT 720
 Db 814 LFSVLYNERARRPGLIGASVGLGDDIHRAMRTVLRADPPPELYFVAVDTGAYDIT 873
 QY 721 PDBRLTEVIASIIKPONTYCVRRYAVVQKAAHGVKAFKSHVSTLTDLPYMRQFVAHL 780
 Db 874 PDBRLTEVIASIIKPONTYCVRRYAVVQKAAHGVKAFKSHVSTLTDLPYMRQFVAHL 933
 QY 781 QETSPLDVAVIESSSLNEASSGLPVEPLRFVCHAVRIRGKSVYOCQGIPOGSLSTL 840
 Db 934 QETSPLDVAVIESSSLNEASSGLPVEPLRFVCHAVRIRGKSVYOCQGIPOGSLSTL 993
 QY 841 LCSTCYGDMENKLFAGIRRDGLLRLVDPDLVTPHLTHAKTELRILVSGVPEYGVNL 900
 Db 994 LCSTCYGDMENKLFAGIRRDGLLRLVDPDLVTPHLTHAKTELRILVSGVPEYGVNL 1053
 QY 901 RKTIVNPFVDEALGTAFFVQMPAHGLFPWCGILLDRTELVOSDYVSARTISIRASLTF 960
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 QY 961 NRGFKAGNRNRKLFVGLRCKHSLFLDLQVNSIQVCTNIYKILLQAVRFACVLOLP 1020
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 QY 1081 KLTRHRRTVYPLIGSLPTAQTQSRKLPGLTTLALEAANPALPSPFKTLLD 1132
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RESULT 33
 US-08-912-951-314
 ; Sequence 314, Application US/08912951
 ; Patent No. 6475789
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: HUMAN TELOWERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 ; NUMBER OF SEQUENCES: 335
 ; THERAPEUTIC METHODS
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/912,951
 ; FILING DATE: 14-AUG-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 314:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1285 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-912-951-314

Query Match 99.8%; Score 5952; DB 4; Length 1285;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPRCRAVNSLSHSHREVLPATFVRRLGPOGMRVYQGDPAAPFALVAQCLVCVPM 60
 Db 154 MRAPRCRAVNSLSHSHREVLPATFVRRLGPOGMRVYQGDPAAPFALVAQCLVCVPM 213
 QY 61 DARPPPAAPSFROYSCLEIYVARVYLQRLCERGAKNVLAFGALLDGAAGPEEFTTSVR 120
 Db 214 DARPPPAAPSFROYSCLEIYVARVYLQRLCERGAKNVLAFGALLDGAAGPEEFTTSVR 273
 QY 121 SYLPNTVTDALRGSGAWGLILRRVQDDVYLHLLARCALFVLVAPSCAYQVCGPPLVQZGA 180
 Db 274 SYLPNTVTDALRGSGAWGLILRRVQDDVYLHLLARCALFVLVAPSCAYQVCGPPLVQZGA 333
 QY 181 ATQARPPPHASGPRRLRCERAMNHSVBAAGVPLGLPAPGARRGGSASRLPLPKPRRR 240
 Db 334 ATQARPPPHASGPRRLRCERAMNHSVBAAGVPLGLPAPGARRGGSASRLPLPKPRRR 393
 QY 241 GAAPPEKTPVGGGMAHGRSTRGSDGFCVSPAPARAEATSLGALSTGRSHSPSVG 300
 Db 394 GAAPPEKTPVGGGMAHGRSTRGSDGFCVSPAPARAEATSLGALSTGRSHSPSVG 453
 QY 301 ROHAGPSTSRPPSPMDTPCPPVYAETKHPLYSGGDKXQLRPSFLSLRPSLTGAARL 360
 Db 454 ROHAGPSTSRPPSPMDTPCPPVYAETKHPLYSGGDKXQLRPSFLSLRPSLTGAARL 513
 QY 361 VETIFLGRPMWPGPRRLPLRPLPORVWOMRPLFELGNHACQGYVLKTHCPRAAVT 420
 Db 514 VETIFLGRPMWPGPRRLPLRPLPORVWOMRPLFELGNHACQGYVLKTHCPRAAVT 573
 QY 421 PAAGVCAEKPOGSAVAPEEEDTDRRLVOLLROHSSFWQYGFVRACLRRLVPPGLMGS 480
 Db 574 PAAGVCAEKPOGSAVAPEEEDTDRRLVOLLROHSSFWQYGFVRACLRRLVPPGLMGS 633
 QY 481 RHNERFLRNKTKFISLGHAKLSLQELTWKSVRDCMILARSBGVGVPAAEHRLKEEI 540

Db 634 RINERREPLNKTSTSLGKHAHLSLOELTWKSVDCMRLRSPOGCVPAHRLREI 693
 QY 541 LAKFLHMLSVYVVELLSFFVYETETQKRLFFRPSWSKLSIGIRHKLXRVOLRE 600
 Db 694 LAKFLHMLSVYVVELLSFFVYETETQKRLFFRPSWSKLSIGIRHKLXRVOLRE 753
 QY 601 LSEAVRQREARPPALTSRLRFLPKPDGLRPIVMDVVGAFPRERREKRLTSRYKA 660
 Db 754 LSEAVRQREARPPALTSRLRFLPKPDGLRPIVMDVVGAFPRERREKRLTSRYKA 813
 QY 661 LFSVNIYERARRPGLLGASVLGLDDIHPAMRTFVLVRAODPPPELYEFKVDVYADTI 720
 Db 814 LFSVNIYERARRPGLLGASVLGLDDIHPAMRTFVLVRAODPPPELYEFKVDVYADTI 873
 QY 721 PODRLTEVASTIKKQNTYCVRRYAVVQKAAAGHRAKPKSHVSTLTLOQYMQPVAHL 780
 Db 874 PODRLTEVASTIKKQNTYCVRRYAVVQKAAAGHRAKPKSHVSTLTLOQYMQPVAHL 933
 QY 781 QETSPLRDAVVIQESSSLNEASSGFDVFLRFMCHAVIRKGSYVQCGI:POGSIISTL 840
 Db 934 QETSPLRDAVVIQESSSLNEASSGFDVFLRFMCHAVIRKGSYVQCGI:POGSIISTL 993
 QY 841 LCSLCYGMENKLPAGIRRDGILLRLVDDFLIVTFLHTAKFTLTVRGVPERGVVNL 900
 Db 994 LCSLCYGMENKLPAGIRRDGILLRLVDDFLIVTFLHTAKFTLTVRGVPERGVVNL 1053
 QY 901 RKTVVNPEVEDALGSTAVQWPAHGLPFMCGILLDTSTLEVOQDYSYASTSRASYTF 960
 Db 1054 RKTVVNPEVEDALGSTAVQWPAHGLPFMCGILLDTSTLEVOQDYSYASTSRASYTF 1113
 QY 961 NEGFAGNMRRKLPGLVRLKCHSLFDLQVNSLQVCTNIYKILLQAYFFHACVQLP 1020
 Db 1114 NEGFAGNMRRKLPGLVRLKCHSLFDLQVNSLQVCTNIYKILLQAYFFHACVQLP 1173
 QY 1021 FHOQWKNTEFLRLYISDTASLCYSILKAKNAGSLGAKGAGLP:PSNAVQMLCHQARLL 1080
 Db 1174 FHOQWKNTEFLRLYISDTASLCYSILKAKNAGSLGAKGAGLP:PSNAVQMLCHQARLL 1233
 QY 1081 KTRRRTVTPPLGSLRTAQTOLSRKLPETTLTALEAANPALP:PSDFITLD 1132
 Db 1234 KTRRRTVTPPLGSLRTAQTOLSRKLPETTLTALEAANPALP:PSDFITLD 1285

RESULT 34
 US-09-402-181B-600
 ; Sequence 600, Application US/09402181B
 ; Patent No. 6610839
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; ; Lingner, Joachim
 ; ; Nakamura, Toru
 ; ; Chapman, Karen B.
 ; ; Morley, Gregg B.
 ; ; Harley, Calvin B.
 ; ; Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 633
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA: US/09/402,181B
 ; APPLICATION NUMBER: US/09/402,181B
 ; FILING DATE: 29-Sep-1997
 ; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ausenbue, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 600:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1285 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1285
 OTHER INFORMATION: /note="fusion protein composed of
 enterokinase cleavable, His tagged
 chloredoxin moiety and full length hTERT"
 SEQUENCE DESCRIPTION: SEQ ID NO: 600:
 US-09-402-181B-600

Query Match 99.8%; Score 5952; DB 4; Length 1285;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPAPRCRAVRSILRSHYREVLPLATFVRRLPGQWRVLYQRDPAAFRALVAQCLVCVM 60
 Db 154 MPAPRCRAVRSILRSHYREVLPLATFVRRLPGQWRVLYQRDPAAFRALVAQCLVCVM 213
 QY 61 DAPPPAAPSFRQVSLCKELVAVVLOQLCERAKNYLARGFALLDQARGPPEAFTTSVR 120
 Db 214 DAPPPAAPSFRQVSLCKELVAVVLOQLCERAKNYLARGFALLDQARGPPEAFTTSVR 273
 QY 121 SYLPNTVTDALRSGAGMLLRVGDVVLHLARCALFVLVAFSCAYOVCGPPLYQLGA 180
 Db 274 SYLPNTVTDALRSGAGMLLRVGDVVLHLARCALFVLVAFSCAYOVCGPPLYQLGA 333
 QY 181 ATQARPPHAGGRRRLGCEBAMNHSVRAGVPLGPAFGARRGGSASRSJPLPRPRR 240
 Db 334 ATQARPPHAGGRRRLGCEBAMNHSVRAGVPLGPAFGARRGGSASRSJPLPRPRR 393
 QY 241 GAAPPEPRTPVGGSMHAGRTGPGSDRGCVVSPAPPAEATSLGALSGTRHSPSVG 300
 Db 394 GAAPPEPRTPVGGSMHAGRTGPGSDRGCVVSPAPPAEATSLGALSGTRHSPSVG 453
 QY 301 ROHHAGPSTSRPPRMDTPCPVVAETGKFLYSSGDKQLRPSFLLSLRPSLTGARLL 360
 Db 454 ROHHAGPSTSRPPRMDTPCPVVAETGKFLYSSGDKQLRPSFLLSLRPSLTGARLL 513
 QY 361 VETIFLGSRPMWCTRRLLPRLPQRYWQMRPLFELILGNHACCPYVLLKTCOPLBAAYT 420
 Db 514 VETIFLGSRPMWCTRRLLPRLPQRYWQMRPLFELILGNHACCPYVLLKTCOPLBAAYT 573

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QY 421 PAAGVACAREKPGQSVAPAEEDIDPRRLVOLLKROHSSPMQVGFVACLRRLVPPGLMGS 480
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QY 481 RHNERRLRLNTKXFIISGKAKLSLOGLTKMSVRCAMLRSPGVCVPAARHRLREEL 540
Db 634 RHNERRLRLNTKXFIISGKAKLSLOGLTKMSVRCAMLRSPGVCVPAARHRLREEL 693
QY 541 LAKEFLHMSVYVVELLSFEFFYTETTFQGNRLFEFFRPSWSXLOSIGIRHOLKRVQRE 600
Db 694 LAKEFLHMSVYVVELLSFEFFYTETTFQGNRLFEFFRPSWSXLOSIGIRHOLKRVQRE 753
QY 601 LSAEVRQREARPAALITSLRLFKPDGLRPIVNDYVGAFTFRERKAEELTSRVXA 660
Db 754 LSAEVRQREARPAALITSLRLFKPDGLRPIVNDYVGAFTFRERKAEELTSRVXA 813
QY 661 LFSVLANERARRRGLGASVGLDDIHRARTVLVRADPPPELXYFVVDVTGAYDTI 720
Db 814 LFSVLANERARRRGLGASVGLDDIHRARTVLVRADPPPELXYFVVDVTGAYDTI 873
QY 721 PODRLTEVIAIIPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDQPYMKQFVAHL 780
Db 874 PODRLTEVIAIIPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDQPYMKQFVAHL 933
QY 781 QETSPLDANYTEBSSSLNEASSGLFDVFLRPMCHAVRIRGKSYYOCQGIPOGSLILSTL 840
Db 934 QETSPLDANYTEBSSSLNEASSGLFDVFLRPMCHAVRIRGKSYYOCQGIPOGSLILSTL 993
QY 841 LCSI.CYGDMMENKLPAGIRRDGLILRLVDDFLVTLPHLTHAKTLRLTVSGVPEYGVNVL 900
Db 994 LCSI.CYGDMMENKLPAGIRRDGLILRLVDDFLVTLPHLTHAKTLRLTVSGVPEYGVNVL 1053
QY 901 RKTYYNPFVEDEALIGTAPVQMPAHGJ.FPWCGJLIDTRTL.EVQSDYSSVARTSIRASVTF 960
Db 1054 RKTYYNPFVEDEALIGTAPVQMPAHGJ.FPWCGJLIDTRTL.EVQSDYSSVARTSIRASVTF 1113
QY 961 NRGFKAGRNMRKLFGLRLKCHSLFLDLQVNSIQTCNTIYKILLLOARFACVLOLP 1020
Db 1114 NRGFKAGRNMRKLFGLRLKCHSLFLDLQVNSIQTCNTIYKILLLOARFACVLOLP 1173
QY 1021 FHQGVNKPTEFFLRVISDLSLACYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1174 FHQGVNKPTEFFLRVISDLSLACYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1233
QY 1081 KLTRHRTYVPLIGSLATAQTQLSRKLPSTTLRLALEAANPALPSPDKTILLD 1132
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RESULT 35
US-09-721-456-600

Sequence 600, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721 456
FILING DATE: 22-NOV-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974, 549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724, 643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844, 419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846, 017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851, 843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854, 050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911, 312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912, 951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915, 503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 600:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1285
OTHER INFORMATION: /note= "fusion protein composed of
enterokinase cleavable, His tagged
thioredoxin moiety and full length hTERT"
SEQUENCE DESCRIPTION: SEQ ID NO: 600:
US-09-721-456-600
Query Match 99.8%; Score 5952; DB 4; Length 1285;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPRARCAVRSLSHREVPLATFVRRLGPOGMRIVQSGDPAFAFALVAQCIVCPV 60
Db 154 MPRARCAVRSLSHREVPLATFVRRLGPOGMRIVQSGDPAFAFALVAQCIVCPV 213
QY 61 DARPPAAPSPFRQVCLKELVARVQLRCERGAKNVLAFFGALLDGAAGGPEAETTSVR 120
Db 214 DARPPAAPSPFRQVCLKELVARVQLRCERGAKNVLAFFGALLDGAAGGPEAETTSVR 273
QY 121 SYLPTVTDALRGSGAMGLLRVGDVYLHLARCALFVVAESCAVQVCGPPVYQGA 180
Db 274 SYLPTVTDALRGSGAMGLLRVGDVYLHLARCALFVVAESCAVQVCGPPVYQGA 333
QY 181 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAGARRRGASASRLPLFKRPRR 240
Db 334 ATQARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAGARRRGASASRLPLFKRPRR 393

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QY 241 GAAPPEERTPVGGSWAHFGRTRGPDGFCVVSPPAPAEATSTSEALSGTRSHSPVG 300
DB 394 GAAPPEERTPVGGSWAHFGRTRGPDGFCVVSPPAPAEATSTSEALSGTRSHSPVG 453
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DB 454 ROHHAAPPTSTPRPMDTCCPPVVAETGHPLYSSGDKQLPSPFLSLSLRSLGAARL 513
QY 361 VETIFLGSSPPMFGTBRRLPRLPQRYWQNRPLFELIGNHAQCPYGVLLKTCPLRAAVT 420
DB 514 VETIFLGSSPPMFGTBRRLPRLPQRYWQNRPLFELIGNHAQCPYGVLLKTCPLRAAVT 573
QY 421 PAAGVARRKPPQGSVAPEEDTDPRLVOLLROHSSPMQVYGFACICRLRYPGGLMS 480
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QY 541 LAEFLHMLSVYVVELLRFPYVETTPQKRLFPYRPSVMSKOSIGIRHLLKRVQURE 600
DB 694 LAEFLHMLSVYVVELLRFPYVETTPQKRLFPYRPSVMSKOSIGIRHLLKRVQURE 753
QY 601 LSEAEVROHREARFALLTSLRLRFPKPDGLRPIVMDYVVGARTPRERKARLTSRYKA 660
DB 754 LSEAEVROHREARFALLTSLRLRFPKPDGLRPIVMDYVVGARTPRERKARLTSRYKA 813
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DB 814 LPSVLNVEARRRPGLIGASVVLGIDITHRAMRTFVLRADPPPELLFYKXDVTCAYDTI 873
QY 721 PODRLTEVASTIKPONTYCVRRYAVVQKAAGHRAKFKSHVSTLTLQPMROFVANH 780
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QY 781 QETSPLRDAVVIQSSSLNEASSGLFDFVLRFMCHAVRIRKSSVYQCGIPQSSILSTL 840
DB 934 QETSPLRDAVVIQSSSLNEASSGLFDFVLRFMCHAVRIRKSSVYQCGIPQSSILSTL 993
QY 841 LCSLCYGDMENTKLPACIRRDGLILRYDDELVTPLTHAKFELTLVRGVEYGCYNL 900
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QY 901 RKTVMFPVEDBALGGTAFVQMPAHGLFPMCGLLDTRTLEVQSDYSSARTSIRASYTF 960
DB 1054 RKTVMFPVEDBALGGTAFVQMPAHGLFPMCGLLDTRTLEVQSDYSSARTSIRASYTF 1113
QY 961 NRGFKAGRMRRKLPFVLRKCHSLFLDQVNSLQVCNIIKILLQAYRPHACVQLP 1020
DB 1114 NRGFKAGRMRRKLPFVLRKCHSLFLDQVNSLQVCNIIKILLQAYRPHACVQLP 1173
QY 1021 FHQCVKNTFTFLRVTSDPASLCYSTLKAKNAGMSLGAAGAPLPSEAVQWLCHQAFLL 1080
DB 1174 FHQCVKNTFTFLRVTSDPASLCYSTLKAKNAGMSLGAAGAPLPSEAVQWLCHQAFLL 1233
QY 1081 KLTRHRVTYVPLIGSLRTAQOLSRKLPSTTVLTALZAAANPALPSDFKTIID 1132
DB 1234 KLTRHRVTYVPLIGSLRTAQOLSRKLPSTTVLTALZAAANPALPSDFKTIID 1285

RESULT 36
US-08-974-549A-5
Sequence 5, Application US/08974549A
Patent No. 6,166,178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linsner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-549A-5

Query Match 67.9%; Score 4046; DB 3; Length 807;
Best Local Similarity 99.9%; Pctd. No. 0;
Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLSHYREVLPATFVRRLPGQGRVLRGDPAPAFRALVACLVQVPM 60
DB 1 MPAPRCRAVRSLLSHYREVLPATFVRRLPGQGRVLRGDPAPAFRALVACLVQVPM 60
QY 61 DAPPPAAPSFRVSCVSKELVAVRLQRCGAKNVLAEGFALLDQARGCPPEAFTTVR 120

Tue Dec 21 15:43:30 2004

us-08-974-584c-118.ra1

Page 39

Db 61 DARPPAASFRQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGPPEATTSVR 120
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Db 121 SYLPTNTVDALRGSGAMGILLRRVGDVYLHLLARCALFVLAAPSCAYQVCGPPLYQGA 180
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Db 181 ATQARPPPHASGPRRLGCEPAMNHSVREAGVPLGAPGARRRGSGASRSLPLPKRPRR 240
Qy 241 GAAPPEERTFVQGGSWAHGRTGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
Db 241 GAAPPEERTFVQGGSWAHGRTGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
Qy 301 ROHAGPSTSRPPMDTCCPVYAETKHFLYSSGDKQLRPSFLSSLRPSLTGARL 360
Db 301 ROHAGPSTSRPPMDTCCPVYAETKHFLYSSGDKQLRPSFLSSLRPSLTGARL 360
Qy 361 VETIFLGSRPWMPGTFRRLPLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPWMPGTFRRLPLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLRQSHSPWQYGFVAPACLRILVPGLMGS 480
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Db 601 LSEAEVQRHREARPPALTSRLRFPRKPDGRPIVNMDDVVGARTPRERKAEELTSRYVA 660
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Db 661 LFSVLYNERARRPGLGASVGLDDHRAWRTVLAARAQDPPELYFVAVDTGAYDTI 720
Qy 721 POBRLTEVIAIITKPONTCVREYAVVQKAAHGHVRAAFKSHV 763
Db 721 POBRLTEVIAIITKPONTCVREYAVVQKAAHGHVRAAFKSHV 763

RESULT 37
US-08-912-951-5
Sequence 5, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-5
Query Match 67.9%; Score 4046; DB 4; Length 807;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MRARPCANVSLRSHREVLPLATFYRRIGPGQMRVYQGDPAFAFALVAQCLVCPW 60
Db 1 MRARPCANVSLRSHREVLPLATFYRRIGPGQMRVYQGDPAFAFALVAQCLVCPW 60
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Qy 121 SYLPTNTVDALRGSGAMGILLRRVGDVYLHLLARCALFVLAAPSCAYQVCGPPLYQGA 180
Db 121 SYLPTNTVDALRGSGAMGILLRRVGDVYLHLLARCALFVLAAPSCAYQVCGPPLYQGA 180
Qy 181 ATQARPPPHASGPRRLGCEPAMNHSVREAGVPLGAPGARRRGSGASRSLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGCEPAMNHSVREAGVPLGAPGARRRGSGASRSLPLPKRPRR 240
Qy 241 GAAPPEERTFVQGGSWAHGRTGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
Db 241 GAAPPEERTFVQGGSWAHGRTGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
Qy 301 ROHAGPSTSRPPMDTCCPVYAETKHFLYSSGDKQLRPSFLSSLRPSLTGARL 360
Db 301 ROHAGPSTSRPPMDTCCPVYAETKHFLYSSGDKQLRPSFLSSLRPSLTGARL 360
Qy 361 VETIFLGSRPWMPGTFRRLPLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPWMPGTFRRLPLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLRQSHSPWQYGFVAPACLRILVPGLMGS 480

421 PAAGVAREKPOGSAVAPEEDTDRRLVQLRQSSPMQYGVFVACLRRLVPPGLWGS 480
QY 481 RHNERFPLNTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERFPLNTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
QY 541 LAKFLMLMSVYVELLSFFVYETTFPOKNLFFRPSVMSKLSIGRHLKXVQURE 600
Db 541 LAKFLMLMSVYVELLSFFVYETTFPOKNLFFRPSVMSKLSIGRHLKXVQURE 600
QY 601 LSEAEVQRHREARFALLTSRLRFPKPDGLRPIVMDYVVGARTFRERKRAERLTSRYKA 660
Db 601 LSEAEVQRHREARFALLTSRLRFPKPDGLRPIVMDYVVGARTFRERKRAERLTSRYKA 660
QY 661 LFSVNLVEERARRRGLLGASVLDGDIHRAMRFVLRVRAQDPPPELYFKVDVTGAYDTI 720
Db 661 LFSVNLVEERARRRGLLGASVLDGDIHRAMRFVLRVRAQDPPPELYFKVDVTGAYDTI 720
QY 721 PQRLTEVLASIIKPNQTYCVRRYAVVQKAAHGHVKAFAKSHV 763
Db 721 PQRLTEVLASIIKPNQTYCVRRYAVVQKAAHGHVKAFAKSHV 763

RESULT 38

US-09-402-181B-5

Sequence 5, Application US/09402181B
Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 06/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 06/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 06/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 06/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 06/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 06/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 06/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausenhus, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-00262005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 807 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-402-181B-5

Query Match 67.3%; Score 4046; DB 4; Length 807;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 DAPPAPADSFRVSCLEIIVARVLCERGAQVLAAGFALLDGAAGCPPEAFTTSYR 120
Db 61 DAPPAPADSFRVSCLEIIVARVLCERGAQVLAAGFALLDGAAGCPPEAFTTSYR 120
QY 121 SYLPNTVTTALRGSGAGWGLLRVGGDVLVHLARCALFVLVAPSCAYVCGPELYQLGA 180
Db 121 SYLPNTVTTALRGSGAGWGLLRVGGDVLVHLARCALFVLVAPSCAYVCGPELYQLGA 180
QY 181 ATQARPPHAGSRRRLGGERAMNSVREAGVPLGIPADGARRGGASASRLPLPKRPR 240
Db 181 ATQARPPHAGSRRRLGGERAMNSVREAGVPLGIPADGARRGGASASRLPLPKRPR 240
QY 241 GAAPPEERTVGGSAHAGRTGPGSDRGFCVSPAPAEATSLLEGALSGRHSHPSG 300
Db 241 GAAPPEERTVGGSAHAGRTGPGSDRGFCVSPAPAEATSLLEGALSGRHSHPSG 300
QY 301 ROHHAGPSTSRPPRMDTPCPVVAETHPLVSSGDKXQLAPSFLLSLRPSLTGARL 360
Db 301 ROHHAGPSTSRPPRMDTPCPVVAETHPLVSSGDKXQLAPSFLLSLRPSLTGARL 360
QY 361 VETIFLGSRPMWGTTRRLPRLPQRYWQMRPLFLELGHNAQCPYGVLLKTCPLRAAT 420
Db 361 VETIFLGSRPMWGTTRRLPRLPQRYWQMRPLFLELGHNAQCPYGVLLKTCPLRAAT 420
QY 421 PAAGVAREKPOGSAVAPEEDTDRRLVQLRQSSPMQYGVFVACLRRLVPPGLWGS 480
Db 421 PAAGVAREKPOGSAVAPEEDTDRRLVQLRQSSPMQYGVFVACLRRLVPPGLWGS 480
QY 481 RHNERFPLNTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERFPLNTKFFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREI 540
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QY 601 LSEAEVQRHREARFALLTSRLRFPKPDGLRPIVMDYVVGARTFRERKRAERLTSRYKA 660
Db 601 LSEAEVQRHREARFALLTSRLRFPKPDGLRPIVMDYVVGARTFRERKRAERLTSRYKA 660
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RESULT 39
US-09-721-456-5
Sequence 5, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cecchi, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-721-456-5
Query Match 67.9%; Score 4046; DB 4; Length 807;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 762; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MPBAPRCVAVSLRSHREVLPLATFVRRLGPGQNRIVQGDPAAPRAVAOCLVCVPM 60
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DB 61 DARPBPAPSFROYSCLEKELVAVLQRCERGANVLAFGFALLDGAAGPPEAFTTSVR 120
QY 121 SYLPNTVTDALRGSGAWGLLRVYDDVYLHARCALFVLVAPSCAYQVCGPPLYQGA 180
DB 121 SYLPNTVTDALRGSGAWGLLRVYDDVYLHARCALFVLVAPSCAYQVCGPPLYQGA 180
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DB 181 ATQAPPPHAGSPRRRLGCEPAMNHSVEACVPLGAPGARRGSGASRSLPLPKRRR 240
QY 241 GAAPPERTPVQGGSWAHPCGTRGSDRGFCVSPAPAEATSLGALSSTRSHPSVG 300
DB 241 GAAPPERTPVQGGSWAHPCGTRGSDRGFCVSPAPAEATSLGALSSTRSHPSVG 300
QY 301 RQHNAGPSTSRPPRPWDTPCPPVYAEKHLFYSGGDEQLRPSTLSLRLPSTGARL 360
DB 301 RQHNAGPSTSRPPRPWDTPCPPVYAEKHLFYSGGDEQLRPSTLSLRLPSTGARL 360
QY 361 VETITLGRPMWPGTFRRLPLRPORWQMRPLFELGNHACCPYGLTKHCPLEAAVT 420
DB 361 VETITLGRPMWPGTFRRLPLRPORWQMRPLFELGNHACCPYGLTKHCPLEAAVT 420
QY 421 PAAGCAREKPGQSVAAPEEDTDBRLVQLLRHSSWQVYGFYACLRLLVPPGLMG 480
DB 421 PAAGCAREKPGQSVAAPEEDTDBRLVQLLRHSSWQVYGFYACLRLLVPPGLMG 480
QY 481 RNNRRPLRNTKFTSLGKAKLSQELTWKMSVDCMWRSPGVGCPAPAEHLRBEI 540
DB 481 RNNRRPLRNTKFTSLGKAKLSQELTWKMSVDCMWRSPGVGCPAPAEHLRBEI 540
QY 541 IAKFLHMLSVYVVELLRSFFVYETTFQKNRLEFYRPSWSKLSQSIROHLKRVQURE 600
DB 541 IAKFLHMLSVYVVELLRSFFVYETTFQKNRLEFYRPSWSKLSQSIROHLKRVQURE 600
QY 601 LSEAEVRQREARPLLTSLRLFIKPDGLRPVMDVVGARTREKRELRSLRYKA 660
DB 601 LSEAEVRQREARPLLTSLRLFIKPDGLRPVMDVVGARTREKRELRSLRYKA 660
QY 661 LFSVLNVERARRPGLGASVGLDDIHRAMRTFVLRAQDPPEPLRYVKVDVTGAYDTI 720
DB 661 LFSVLNVERARRPGLGASVGLDDIHRAMRTFVLRAQDPPEPLRYVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIKPONTYCVRRYAVVQKAAGHVRKAFKSHV 763
DB 721 PODRLTEVIASIKPONTYCVRRYAVVQKAAGHVRKAFKSHV 763

RESULT 40
US-08-851-843A-217
Sequence 217, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cecchi, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
City: San Francisco
STATE: California
COUNTRY: United States of America


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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-8200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-851-843A-217

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Best Local Similarity 78.5%; Pred. No. 0;
Matches 786; Conservative 24; Mismatches 124; Indels 67; Gaps 18;

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DB      39 APTXCAGRRRC-----TSSALXLRP-----GPRHTLXDPXASGIORAMNSVREAGVPLG 87

QY      216 LPAPGARRRGSGASRSLPLPK3PR-RGAAPPERT--PVGGSMWHPGRTT-RGSDRGFC 271
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      88 CQ---PRVAGGAGAPPAEVCRCPRGPGVALPLSSGRPLGRG---PGPTRAGRLDR-VT 139

QY      272 VVS-----PARP-----ABEATSLGALSGTRSHSPVGRQ--HHAGPPSTSRP 313
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      140 VVSVMCHLPDPKPKPLMVRSLARATPTHPMAASTTRAHPHGHVGLHALSPGVR- 198

QY      314 PRPWDTCPBPVYAEKTHFLYSSGDKQLRPSFLSLSPILTGARLYETIFLGRPMMP 373
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      199 ----DQADLLLRROXHC-----XPPSYST-YLPSLTLGVREVGDXLISGRPMMP 244

QY      374 GTPRRRLPRLPORWQWRPLFELILGNHACQPYGLK--THCPLEAATVPAAGVACAREXP 431
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      245 GPPAGCPACPSXTKGCGPCFWSCLGTTTSAPFGCSSRRTRARCELRSPQSPVS--VPGSRP 302

QY      432 QGSVAAPREEDTDPRLVOLLROHSSPWQVYGFVACLRILVPPGLMGSRNERRFLNLT 491
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      303 RALMWRPPRRRNTDPRRLVOLLROHSSPWQVYGFVACLRILVPPGLMGSRNERRFLNLT 362

QY      492 KKFISLIGKIAKLSLOELTWKMSVRCAMLRSPGVGCVPAAEHRLREELILAKFLHMLMSV 551
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      363 KKFISLIGKIAKLSLOELTWKMSVRCAMLRSPGVGCVPAAEHRLREELILAKFLHMLMSV 422

QY      552 YVEELLRSFFVYETTFQGNRLFYRPSVWSKLOSIGIRQHKRVQLRELSEAEVRQRE 611
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      423 YVEELLRSFFVYETTFQGNRLFYRPSVWSKLOSIGIRQHKRVQLRELSEAEVRQRE 482

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QY      612 ARPALLTSRLRFIPKPDGLRPIVMNDVVGARTFREREKREKRLTSRYKALFSVLYNERAR 671
DB      483 ARPALLTSRLRFIPKPDGLRPIVMNDVVGARTFREREKREKRLTSRYKALFSVLYNERAR 542

QY      672 RPLGLGASVGLDDIHNAMRTFVLRYRAQDPPELIFVKVDYGAADTLPODLTEVIAS 731
DB      543 RPLGLGASVGLDDIHNAMRTFVLRYRAQDPPELIFVKVDYGAADTLPODLTEVIAS 602

QY      732 IIPQNTYCVRRYAVVQKAHGHVRAKFSHVSITLDLPYMEQFVAHLQETSPLDAVY 791
DB      603 IIPQNTYCVRRYAVVQKAHGHVRAKFSHVSITLDLPYMEQFVAHLQETSPLDAVY 662

QY      792 IEQSSSINENASSGLFDVFLRFMCHAVRIQKSYVOQGIPOGSIITLCLCYGDMEN 851
DB      663 IEQSSSINENASSGLFDVFLRFMCHAVRIQKSYVOQGIPOGSIITLCLCYGDMEN 722

QY      852 KLFAGIRDDGLRLVYDPLVTPHILTHAKTFLRTLVRGVPEYGVNLRKTYVNPVED 911
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DB      783 EALGTAFFVQMPAHGLFPWCGLLLDTRTLEVOGSDYSSVARTSIRASVTNRGFKAGRNR 842

QY      972 RKLPGVIRLKGSLFLIDQVNSIQVCTNIYKILLQAYRFACTVQLEPHQVWKNUPTE 1031
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QY      1032 FLRVISDTASLCYSIIKAKNAGMSLGAKAGPLPSEAVQWLMCHOAFLIKLTRHRTYVP 1091
DB      903 FLRVISDTASLCYSIIKAKNAGMSLGAKAGPLPSEAVQWLMCHOAFLIKLTRHRTYVP 962

QY      1092 LLSISRTAQQLSRKLPGLTTLTLEAANPALBSPDKTILD 1132
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Job time : 66 secs

Tue Dec 21 15:43:31 2004

us-08-974-584c-118.rapb

Page 1

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: December 20, 2004, 15:56:51 ; Search time 166 Seconds

(without alignments)
2440.176 Million cell updates/sec

Title: US-08-974-584C-118

Perfect score: 5963
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Gapop 10.0 , Gapext 0.5

Searched: 1589859 seqs, 357834939 residues

Total number of hits satisfying chosen parameters: 1589859

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 120 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/prodata/1/pubppaa/PCN_NEW_PUB.pep:*
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- 20: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	5963	100.0	1132	17	US-10-877-022-344
4	5963	100.0	1407	14	US-10-044-692-334
5	5963	100.0	1407	14	US-10-044-539-334
6	5963	100.0	1407	14	US-10-325-810-628
7	5963	100.0	1407	17	US-10-877-124-628
8	5963	100.0	1407	17	US-10-877-022-628
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11	5952	99.8	1132	9	US-09-843-676-225
12	5952	99.8	1132	9	US-09-953-052-2
13	5952	99.8	1132	11	US-09-788-110A-23
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22	5952	99.8	1132	14	US-10-388-578-2
23	5952	99.8	1132	16	US-10-602-441-2
24	5952	99.8	1132	16	US-10-389-431-2
25	5952	99.8	1132	16	US-10-877-124-2
26	5952	99.8	1132	17	US-10-877-022-2
27	5952	99.8	1132	17	US-10-877-022-2
28	5952	99.8	1154	14	US-10-044-692-323
29	5952	99.8	1154	14	US-10-044-539-323
30	5952	99.8	1154	14	US-10-325-810-611
31	5952	99.8	1154	17	US-10-877-124-611
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33	5952	99.8	1189	14	US-10-044-692-325
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35	5952	99.8	1189	14	US-10-325-810-613
36	5952	99.8	1189	17	US-10-877-124-613
37	5952	99.8	1189	17	US-10-877-022-613
38	5952	99.8	1200	14	US-10-044-692-324
39	5952	99.8	1200	14	US-10-044-539-324
40	5952	99.8	1200	17	US-10-877-124-612
41	5952	99.8	1200	17	US-10-877-022-612
42	5952	99.8	1285	14	US-10-044-692-314
43	5952	99.8	1285	14	US-10-325-810-600
44	5952	99.8	1285	14	US-10-044-539-314
45	5952	99.8	1285	17	US-10-877-124-600
46	5952	99.8	1285	17	US-10-877-022-600
47	5952	99.8	1285	17	US-10-385-882-2
48	5945	99.7	1132	16	US-10-602-441-12
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50	4046	67.9	807	14	US-10-044-539-5
51	4046	67.9	807	14	US-10-325-810-5
52	4046	67.9	807	17	US-10-877-124-5
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57	3810.5	63.9	1003	14	US-10-054-295-217
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66	2861	43.3	500	14	US-10-282-960-81
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68	2178	36.5	438	14	US-10-294-778-10
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71	2163.5	36.3	437	14	US-10-602-441-10
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83	1565	26.2	538	14	US-10-044-692-316
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85	1565	26.2	538	14	US-10-325-810-602
86	1565	26.2	538	17	US-10-877-124-602

87 1565 26.2 538 17 US-10-877-022-602 Sequence 602, App
 88 1506 25.3 514 14 US-10-044-692-319 Sequence 319, App
 89 1506 25.3 514 14 US-10-044-539-319 Sequence 319, App
 90 1506 25.3 514 14 US-10-325-810-605 Sequence 605, App
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 92 1506 25.3 514 17 US-10-877-022-605 Sequence 605, App
 93 1484 24.9 291 14 US-10-282-960-3 Sequence 3, Appl
 94 1454 24.4 517 14 US-10-044-692-320 Sequence 320, App
 95 1454 24.4 517 14 US-10-044-539-320 Sequence 320, App
 96 1454 24.4 517 14 US-10-325-810-606 Sequence 606, App
 97 1454 24.4 517 17 US-10-877-124-606 Sequence 606, App
 98 1454 24.4 517 17 US-10-877-022-606 Sequence 606, App
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 103 1447 24.3 530 17 US-10-877-022-603 Sequence 603, App
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 106 1386 23.2 515 14 US-10-044-539-318 Sequence 318, App
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 109 1386 23.2 515 17 US-10-877-022-604 Sequence 604, App
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 111 1243.5 20.9 364 14 US-10-304-095-41 Sequence 41, Appl
 112 1090 18.3 259 14 US-10-044-692-10 Sequence 10, Appl
 113 1090 18.3 259 14 US-10-044-539-10 Sequence 10, Appl
 114 1090 18.3 259 14 US-10-325-810-10 Sequence 10, Appl
 115 1090 18.3 259 17 US-10-877-124-10 Sequence 10, Appl
 116 1090 18.3 259 17 US-10-877-022-10 Sequence 10, Appl
 117 929 15.6 222 9 US-09-843-676-202 Sequence 202, App
 118 929 15.6 222 14 US-09-438-486-202 Sequence 202, App
 119 929 15.6 222 14 US-10-053-758-202 Sequence 202, App
 120 929 15.6 222 14 US-10-054-295-202 Sequence 202, App

ALIGNMENTS

RESULT 1
 US-10-325-810-344
 Sequence 344, Application US/10325810
 Publication No. US20030204069A1

GENERAL INFORMATION:

APPLICANT:

Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181

FILING DATE: 29-Sep-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ausenhus, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 344:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 344:
 US-10-325-810-344

Query Match 100.0%; Score 5963; DB 14; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCAVRSILRSYREVLPLATFVRRLGQGRVLYQGDPAFRAVLAQCLVCPW 60
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 DB 61 DARPAPAPSFROVSCIKELVAVYVRLQRCERKANVLAAGFALLDGRGCPPEAFTTSR 120
 QY 121 SYLPNTVTDLRSGAGWLLIRVGGDVLVHLARCALFVLVAPSCAYVCGPPLYQLGA 180
 DB 121 SYLPNTVTDLRSGAGWLLIRVGGDVLVHLARCALFVLVAPSCAYVCGPPLYQLGA 180
 QY 181 ATQARPPHAGGRRLGCEERANVSVREAGVPLGPAFGARRGGSASRSLLPPRRR 240
 DB 181 ATQARPPHAGGRRLGCEERANVSVREAGVPLGPAFGARRGGSASRSLLPPRRR 240
 QY 241 GAAPPEPRTPVGGSAHAPRTGSPDRGCVVSPARPEATSLGALSGTRHSPVG 300
 DB 241 GAAPPEPRTPVGGSAHAPRTGSPDRGCVVSPARPEATSLGALSGTRHSPVG 300
 QY 301 ROHHAGPPSTRPPEPMDTCCPVVAETKHFLYSSGDKQLPSPFLSLRSLTGARL 360
 DB 301 ROHHAGPPSTRPPEPMDTCCPVVAETKHFLYSSGDKQLPSPFLSLRSLTGARL 360
 QY 361 VETIFIGSRPMWGTFRRLPLPQRYWQRPFLFLSLGHAQCPYVLLKTCPLRAAT 420
 DB 361 VETIFIGSRPMWGTFRRLPLPQRYWQRPFLFLSLGHAQCPYVLLKTCPLRAAT 420
 QY 421 PAAGVCAREKQSVAPAEEDTDPRRLVQLRQHSPPQVYGFVACLRRLVPPGIMS 480
 DB 421 PAAGVCAREKQSVAPAEEDTDPRRLVQLRQHSPPQVYGFVACLRRLVPPGIMS 480
 QY 481 RHNERPRRLNTKFKISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAHRLREI 540
 DB 481 RHNERPRRLNTKFKISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAHRLREI 540

QY 541 LAKPLHMLSVYVYELLRSFFYTETTFOKNRLFFVPSVMSKLOSIGIRQHLKRYOLRE 600
 DB 541 LAKPLHMLSVYVYELLRSFFYTETTFOKNRLFFVPSVMSKLOSIGIRQHLKRYOLRE 600
 QY 601 LSEAVERQHEARPAALLTSRLRFLPKPDGLRPVNMDDYVGAFTFRREKKAERLTSRYVA 660
 DB 601 LSEAVERQHEARPAALLTSRLRFLPKPDGLRPVNMDDYVGAFTFRREKKAERLTSRYVA 660
 QY 661 LFSVLANERARRPGLLGSVGLDDIRHARMTFLVRADDPPELTFVAVDVGADTI 720
 DB 661 LFSVLANERARRPGLLGSVGLDDIRHARMTFLVRADDPPELTFVAVDVGADTI 720
 QY 721 PODRLTEVIAIIRKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 DB 721 PODRLTEVIAIIRKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPLRDYAVIEQSSSLNEASSGLFVFLRPMCHAVRIRKGSYVOCQIGPOGSIISTL 840
 DB 781 QETSPLRDYAVIEQSSSLNEASSGLFVFLRPMCHAVRIRKGSYVOCQIGPOGSIISTL 840
 QY 841 LCSLCYGDMEKRLPAGLRDGLRLVDDFLVTPHILTHAKTFLRLVREVPYGCYVNL 900
 DB 841 LCSLCYGDMEKRLPAGLRDGLRLVDDFLVTPHILTHAKTFLRLVREVPYGCYVNL 900
 QY 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPMCGLLIDRTLEVOSSVARTSIRASVTF 960
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 QY 961 NRGFKARNRMRKLFGLVRLKCHSLFLDQVNSIQTCNTNIXKLLLOARFHAQVLOLP 1020
 DB 961 NRGFKARNRMRKLFGLVRLKCHSLFLDQVNSIQTCNTNIXKLLLOARFHAQVLOLP 1020
 QY 1021 FHQGVNKPTEFFLVISDTASTLCYSILKAKAGMSLAKAGAGLPSEAVQWLCHQAFLL 1080
 DB 1021 FHQGVNKPTEFFLVISDTASTLCYSILKAKAGMSLAKAGAGLPSEAVQWLCHQAFLL 1080
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 DB 1081 KLTHRRVTVYVPLLSLRTAQQLSRKLPGTTLLLEAANPALPSDKITLD 1132

RESULT 2
 US-10-877-124-344
 Sequence 344, Application US/10877124
 Publication No. US20040242529A1
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Linsgner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morita, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/877,124
 FILING DATE: 24-Jun-2004
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999
 APPLICATION NUMBER: 08/974,549
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-May-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-Oct-1997
 APPLICATION NUMBER: WO PCT/US97/17685
 FILING DATE: 01-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 344:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 344:
 US-10-877-124-344

Query Match 100.0%; Score 5963; DB 17; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MPRAPCRAVRSLRSHRYEVLPATFVRRLQPGCMRLVORDDPAFPAVLAQCLVCPM 60
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 DB 61 DARPPAASFRQVSCIKELVARVQLICERGAQVLAFGALLDGAAGGPEAFTTSVR 120
 QY 121 SYLPTNTDALRGSGAMGLLRVGDDVYLHLLARCALFVLAAPSCAYOVGPPLYOQA 180
 DB 121 SYLPTNTDALRGSGAMGLLRVGDDVYLHLLARCALFVLAAPSCAYOVGPPLYOQA 180
 QY 181 ATOAPPPIHAGSPRRRLGGERAMNSVREAGVPLGLPAAGARRGSGASRSLLPKRPR 240
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 DB 241 GAAPPEERTPVQGSMAHNGRTGRGSDGFCVYSAPPAEATSLGALSGTRHSHPSVG 300
 QY 301 ROHHAAPPSTSRPPRMDPCPPVYAETKHFYSSGDKQOLPSSLRLPSLTGAARL 360
 DB 301 ROHHAAPPSTSRPPRMDPCPPVYAETKHFYSSGDKQOLPSSLRLPSLTGAARL 360
 QY 361 VETIFLGSRRPMGPTRRLRPLPORYWQMRPLFLLGNHAQCPYGVLLKTHCPRAAYT 420
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 QY 421 PAAGVCARPKPGSGVAAPPEEDTDPRRLVQLRQSSPMQVGFYRACLRLLVPPGLWGS 480
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QY	481	RHNERRLRNTKKEFISLGNHAKLSLOELTWKMSVNDCKMLRSPGVGCVPAERHRLREE	5400
Db	481	RHNERRLRNTKKEFISLGNHAKLSLOELTWKMSVNDCKMLRSPGVGCVPAERHRLREE	5400
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Db	541	LAKFLHMLSVYVVELLRSEFPYVTEFTFOKRLFFPYRSPVSKUSQISIGIRHLKRYOLRE	6000
QY	601	LSESEVRQRREARFALLTSLRLRFFIPRPODLRPIVNMDEVVGARFFRREKAEELTSVKA	6600
Db	601	LSESEVRQRREARFALLTSLRLRFFIPRPODLRPIVNMDEVVGARFFRREKAEELTSVKA	6600
QY	661	LFESVLYNERRRRREGLLGASVTLGHDIDIRAMRFFVLRVAADOPPELIFYKADVTGADTI	7200
Db	661	LFESVLYNERRRRREGLLGASVTLGHDIDIRAMRFFVLRVAADOPPELIFYKADVTGADTI	7200
QY	721	PODLRLTEVLAIIKPNQNTYCVRRYAVVOXKAHGHVREKAFKSHVSTLTDLOPYMRQFYAHL	7800
Db	721	PODLRLTEVLAIIKPNQNTYCVRRYAVVOXKAHGHVREKAFKSHVSTLTDLOPYMRQFYAHL	7800
QY	781	QETSPLRDVAIVEQSSLSNEASSGFPDVLFRMCHAVRIRGKSVYVOOQGIPOSSILSTL	8400
Db	781	QETSPLRDVAIVEQSSLSNEASSGFPDVLFRMCHAVRIRGKSVYVOOQGIPOSSILSTL	8400
QY	841	LCSLCYGDMENKLFAGIRRDGILLRLVDFLLVTEHLTHARTFLRTIVRGVPEXGVNVL	9000
Db	841	LCSLCYGDMENKLFAGIRRDGILLRLVDFLLVTEHLTHARTFLRTIVRGVPEXGVNVL	9000
QY	901	RKTVVAPPEDELLGSTAFVQMPAHGPFMCGLLDTFTLEVOGDSYSYARTSRASVTF	9600
Db	901	RKTVVAPPEDELLGSTAFVQMPAHGPFMCGLLDTFTLEVOGDSYSYARTSRASVTF	9600
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QY	1021	FHOQVKNPFFPFRVLSIDTASLCYSILKAKAKNGSLGAKKAAGPLSEBAVQMLCHQAFLL	1080
Db	1021	FHOQVKNPFFPFRVLSIDTASLCYSILKAKAKNGSLGAKKAAGPLSEBAVQMLCHQAFLL	1080
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Db	1081	KLFRHRVTYVPLIGSLRTAQOTLSKRLPQTITLLEAANPALPSDEKTIID 1132	
RESULT 3			
US-10-877-022-344			
Sequence 344, Application US/10877022			
Publication No. US20040247613A1			
GENERAL INFORMATION:			
APPLICANT: Cecch, Thomas R.			
Lingner, Joachim			
Nakamura, Toru			
Chapman, Karen B.			
Morin, Gregg B.			
Harley, Calvin B.			
Andrews, William H.			
TITLE OF INVENTION: Human Telomerase Catalytic Subunit			
NUMBER OF SEQUENCES: 727			
CORRESPONDENCE ADDRESS:			
ADDRESS: Townsend and Townsend and Crew LLP			
STREET: Two Embarcadero Center, Eighth Floor			
CITY: San Francisco			
STATE: California			
COUNTRY: USA			
ZIP: 94111-3834			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/10/877,022			

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1 FILING DATE: 24-Jun-2004
2 CLASSIFICATION: <Unknown>
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: US/09/432,503
5 FILING DATE: 02-Nov-1999
6 APPLICATION NUMBER: 08/974,549
7 FILING DATE: <Unknown>
8 APPLICATION NUMBER: US 08/844,419
9 FILING DATE: 18-Apr-1997
10 APPLICATION NUMBER: US 08/846,017
11 FILING DATE: 25-Apr-1997
12 APPLICATION NUMBER: US 08/851,843
13 FILING DATE: 06-May-1997
14 APPLICATION NUMBER: US 08/854,050
15 FILING DATE: 09-May-1997
16 APPLICATION NUMBER: US 08/911,312
17 FILING DATE: 14-Aug-1997
18 APPLICATION NUMBER: US 08/912,951
19 FILING DATE: 14-Aug-1997
20 APPLICATION NUMBER: US 08/915,503
21 FILING DATE: 14-Aug-1997
22 APPLICATION NUMBER: MO PCT/US97/17618
23 FILING DATE: 01-Oct-1997
24 APPLICATION NUMBER: MO PCT/US97/17885
25 FILING DATE: 01-Oct-1997
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Apple, Randipn Ted
28 REGISTRATION NUMBER: 36,429
29 REFERENCE/DOCKET NUMBER: 015389-002610US
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (415) 576-0200
32 TELEFAX: (415) 576-0300
33 INFORMATION FOR SEQ ID NO: 344:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 1132 amino acids
36 TYPE: amino acid
37 TOPOLOGY: linear
38 MOLECULE TYPE: protein
39 SEQUENCE DESCRIPTION: SEQ ID NO: 344:
40
41 US-10-877-022-344
42
43 Query Match 100.0%; Score 5963; DB 17; Length 1132;
44 Best Local Similarity 100.0%; Pred. No. 0;
45 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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47 QY 1 MPRAAPRCAGVSLRSHRYEVLPLATFPRRIGPGQWRLVQGRDPAAFPALVAOCLVCVPM 60
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50 Db 61 DAREPPAASFRQVSCIKELVARVLQRLCEFGANVLAFGALLIDGARGPEAFTTSVR 120
51 QY 121 SYLNTVTDALRSGGAWGLLRVGDVVLVHLARCALFVLVAPSCAYQVCGPPLYOLGA 180
52 Db 121 SYLNTVTDALRSGGAWGLLRVGDVVLVHLARCALFVLVAPSCAYQVCGPPLYOLGA 180
53 QY 121 SYLNTVTDALRSGGAWGLLRVGDVVLVHLARCALFVLVAPSCAYQVCGPPLYOLGA 180
54 Db 121 SYLNTVTDALRSGGAWGLLRVGDVVLVHLARCALFVLVAPSCAYQVCGPPLYOLGA 180
55 QY 181 ATQARPPHASGPPRRRLGCEPAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPR 240
56 Db 181 ATQARPPHASGPPRRRLGCEPAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPR 240
57 QY 181 ATQARPPHASGPPRRRLGCEPAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPR 240
58 Db 181 ATQARPPHASGPPRRRLGCEPAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPR 240
59 QY 241 GAABEPRTPIVQGSMAHPGRTGRPSDQRCVVSAPAPAEATSLLEGALSGTRSHSPVG 300
60 Db 241 GAABEPRTPIVQGSMAHPGRTGRPSDQRCVVSAPAPAEATSLLEGALSGTRSHSPVG 300
61 QY 301 ROHHAGPSTSRPRPMDTCPPIVYAEATKHFLYSSGDKCOLRPSFLLSLRPSLTGARL 360
62 Db 301 ROHHAGPSTSRPRPMDTCPPIVYAEATKHFLYSSGDKCOLRPSFLLSLRPSLTGARL 360
63 QY 361 VETIFLGRPMMPGTPRRLPLPORYOMRPLFLLELGNHAQCYGVLLKXHCPLRAVLT 420
64 Db 361 VETIFLGRPMMPGTPRRLPLPORYOMRPLFLLELGNHAQCYGVLLKXHCPLRAVLT 420
65 QY 361 VETIFLGRPMMPGTPRRLPLPORYOMRPLFLLELGNHAQCYGVLLKXHCPLRAVLT 420
66 Db 361 VETIFLGRPMMPGTPRRLPLPORYOMRPLFLLELGNHAQCYGVLLKXHCPLRAVLT 420

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QY 421 PAAGVCAAREKPOGSAVAPEEDTDPRRLVOLLRQHSSEPMQYGVFVACLRRLVPPGLMGS 480
 Db 421 PAAGVCAAREKPOGSAVAPEEDTDPRRLVOLLRQHSSEPMQYGVFVACLRRLVPPGLMGS 480
 QY 481 RHNRERRRLRTKKTISIGKIAKSLQELTWKMSVRCAMLRSPGVCVPAABHRLREET 540
 Db 481 RHNRERRRLRTKKTISIGKIAKSLQELTWKMSVRCAMLRSPGVCVPAABHRLREET 540
 QY 541 LAKELHLMMSYVVELLRSFFVYVETETFOKNRLFFYRPSWSKLOSGIGIQLKRYOLRE 600
 Db 541 LAKELHLMMSYVVELLRSFFVYVETETFOKNRLFFYRPSWSKLOSGIGIQLKRYOLRE 600
 QY 601 LSEAEVQOHRREARPAALITSLRFLPKPDGLRPIVMDYVVGARTFRREKAEELTSVKA 660
 Db 601 LSEAEVQOHRREARPAALITSLRFLPKPDGLRPIVMDYVVGARTFRREKAEELTSVKA 660
 QY 661 LFSVLNTERARRPCLLGASVGLDDIRHAWRTFVLARADDPPELTVFVVDVTGAYDTI 720
 Db 661 LFSVLNTERARRPCLLGASVGLDDIRHAWRTFVLARADDPPELTVFVVDVTGAYDTI 720
 QY 721 PODRLTEVIASIIKPONTYCVRYAVVQKAAHGHVRAKAFKSHVSTLTDLPYMRQFVAHL 780
 Db 721 PODRLTEVIASIIKPONTYCVRYAVVQKAAHGHVRAKAFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPFLRDVAVIEOSSSLINENASGCLFVFLRFPMCHAVRIKGSYVOCQGIPOGSLISTL 840
 Db 781 QETSPFLRDVAVIEOSSSLINENASGCLFVFLRFPMCHAVRIKGSYVOCQGIPOGSLISTL 840
 QY 841 LCSLCYGMENKLFAGIRRDGLILRLVDDFLVLPPLTHAKTFLRLTVRGVPEYGCVMN 900
 Db 841 LCSLCYGMENKLFAGIRRDGLILRLVDDFLVLPPLTHAKTFLRLTVRGVPEYGCVMN 900
 QY 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPMCGILLDTLREVOGSDYSVARTSIRASVTF 960
 Db 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPMCGILLDTLREVOGSDYSVARTSIRASVTF 960
 QY 961 NRGFKAGRMNRKLFGLVRLKCHSLFLDLQVNSIQYCTNIVYILLQARHFACVLOLP 1020
 Db 961 NRGFKAGRMNRKLFGLVRLKCHSLFLDLQVNSIQYCTNIVYILLQARHFACVLOLP 1020
 QY 1021 FHQGVNKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
 Db 1021 FHQGVNKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
 QY 1081 KLTRHRRTVYPLGLSLTAQTOLSRKLPGLTLTLEAANPALPSPDKTILLD 1132
 Db 1081 KLTRHRRTVYPLGLSLTAQTOLSRKLPGLTLTLEAANPALPSPDKTILLD 1132

RESULT 4
 US-10-044-692-334
 Sequence 334, Application US/10044692
 Publication No. US20030096344A1
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Linsner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 THERAPEUTIC METHODS
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: PatentIn Release #1.0, Version #1.30
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/10/044,692
 ? FILING DATE: 11-Jan-2002
 ? CLASSIFICATION: <Unknown>
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/912,951
 ? FILING DATE: <Unknown>
 ? APPLICATION NUMBER: US 08/854,050
 ? FILING DATE: 09-MAY-1997
 ? APPLICATION NUMBER: US 08/851,843
 ? FILING DATE: 06-MAY-1997
 ? APPLICATION NUMBER: US 08/846,017
 ? FILING DATE: 25-APR-1997
 ? APPLICATION NUMBER: US 08/844,419
 ? FILING DATE: 18-APR-1997
 ? APPLICATION NUMBER: US 08/724,643
 ? FILING DATE: 01-OCT-1996
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Apple, Randolph T.
 ? REGISTRATION NUMBER: 36,429
 ? REFERENCE/DOCKET NUMBER: 015389-002600US
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (415) 576-0200
 ? TELEFAX: (415) 576-0300
 ? INFORMATION FOR SEQ ID NO: 334:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1407 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: <Unknown>
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? SEQUENCE DESCRIPTION: SEQ ID NO: 334:
 US-10-044-692-334
 Query Match 100.0%; Score 5963; DB 14; Length 1407;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRAPRCAGVBSILASHYREVLPATFVYRRLGPOGMRVLVQSGDPAAPFALVAQCICVPM 60
 Db 276 MRAPRCAGVBSILASHYREVLPATFVYRRLGPOGMRVLVQSGDPAAPFALVAQCICVPM 335
 QY 61 DARPPAAPSPFQVSCLELYAVYLQRLCEGAKXVLAFGALLDGAAGPPEAFTTSVR 120
 Db 336 DARPPAAPSPFQVSCLELYAVYLQRLCEGAKXVLAFGALLDGAAGPPEAFTTSVR 395
 QY 121 SYLENTVTDALRGSGAMGLLRRVGDVVLVHLARCALFVLVAPSCAOVCGPPLYOIGA 180
 Db 396 SYLENTVTDALRGSGAMGLLRRVGDVVLVHLARCALFVLVAPSCAOVCGPPLYOIGA 455
 QY 181 ATOARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRRGSASRLPLPKRPRR 240
 Db 456 ATOARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRRGSASRLPLPKRPRR 515
 QY 241 GAAPPERTPVQGGWAPRGTRGSDRGFCVVSAPARAEDATSLGALSGTRHSHPSVG 300
 Db 516 GAAPPERTPVQGGWAPRGTRGSDRGFCVVSAPARAEDATSLGALSGTRHSHPSVG 575
 QY 301 RQHAAGPSTSRPPPMOTPCPPVYAEKHFYLSGDKQOLRPSFLSSLRPSLTGARRL 360
 Db 576 RQHAAGPSTSRPPPMOTPCPPVYAEKHFYLSGDKQOLRPSFLSSLRPSLTGARRL 635
 QY 636 VETIFLGSRPMPWPGTFRPLPLPQRYWQMRPLFELLGNHACPPGVILKTHCPRAAVT 695
 Db 421 PAAGVCAAREKPOGSAVAPEEDTDPRRLVOLLRQHSSEPMQYGVFVACLRRLVPPGLMGS 480
 Db 696 PAAGVCAAREKPOGSAVAPEEDTDPRRLVOLLRQHSSEPMQYGVFVACLRRLVPPGLMGS 755

481 RHNERFLNTKFKISLGKAKLSLOELTWKMSVBDCAMLRRSPGVGCVPAEHRLEBEI 540
756 RHNERFLNTKFKISLGKAKLSLOELTWKMSVBDCAMLRRSPGVGCVPAEHRLEBEI 815
541 LAKFLHMSYVVELLSFFVYETTTPOXNLFYRPSWSKLOSLGIRHLEKRVQURE 600
816 LAKFLHMSYVVELLSFFVYETTTPOXNLFYRPSWSKLOSLGIRHLEKRVQURE 875
601 LSAEVRORREARPAALTSRLRFIPKPDLPVNMDDYVGARTFRREKRAERLSRKA 660
876 LSAEVRORREARPAALTSRLRFIPKPDLPVNMDDYVGARTFRREKRAERLSRKA 935
661 LBSVLNVEARPPGLIGASVIGLDTIHRAMRTFVRPAODPPPELVKVDVTGAYDTI 720
936 LBSVLNVEARPPGLIGASVIGLDTIHRAMRTFVRPAODPPPELVKVDVTGAYDTI 995
721 PDORLETVASIIKPNNTCVARVAVVOCAAHGVRKAFKSVSTLTLOPMRQFVAHL 780
996 PDORLETVASIIKPNNTCVARVAVVOCAAHGVRKAFKSVSTLTLOPMRQFVAHL 1055
781 QETSPRLDAVIEOSSSLNEASSGLFDVFLRPMCHAVRIRGKSYVOCGIPQGSILSTL 840
1056 QETSPRLDAVIEOSSSLNEASSGLFDVFLRPMCHAVRIRGKSYVOCGIPQGSILSTL 1115
841 LGSICYGDMENKLFAGIRDDGLLVLVDPELLVTHAKTEFLTVRGVPEVCVNL 900
1116 LGSICYGDMENKLFAGIRDDGLLVLVDPELLVTHAKTEFLTVRGVPEVCVNL 1175
901 RKTIVNFPVEDBALGGTAFCVMPAHGLFPMCGLLDTRTLEVOQSYSSVARTSIRASTVF 960
1176 RKTIVNFPVEDBALGGTAFCVMPAHGLFPMCGLLDTRTLEVOQSYSSVARTSIRASTVF 1235
961 NRGFKAGNRMRKLFQVFLKCHSLFLDIQVNSLQTCVNTIKILLQAYRPHACVLOLF 1020
1236 NRGFKAGNRMRKLFQVFLKCHSLFLDIQVNSLQTCVNTIKILLQAYRPHACVLOLF 1295
1021 FHOQVKNPTFFLRVSDPASLCYSILKAKNAGMSLGAAGAPLPSBAVWLCHQAPL 1080
1296 FHOQVKNPTFFLRVSDPASLCYSILKAKNAGMSLGAAGAPLPSBAVWLCHQAPL 1355
1081 KLRHRVTYVPLLSLRTAQOLSRKLPQTTLTALBAANPALPSDFXTIID 1132
1356 KLRHRVTYVPLLSLRTAQOLSRKLPQTTLTALBAANPALPSDFXTIID 1407

RESULT 5
US-10-044-539-334
Sequence 334, Application US/10044539
Publication No. US2003010093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044, 539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912, 951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854, 050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851, 843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846, 017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844, 419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724, 643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 334:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 334:
US-10-044-539-334
Query Match 100.0%; Score 5963; DB 14; Length 1407;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MPRAFCRAVSLIRSHYREVLPATFVRRLGPGQWLYVQGDPAFRAVLAQCVCVPM 60
276 MPRAFCRAVSLIRSHYREVLPATFVRRLGPGQWLYVQGDPAFRAVLAQCVCVPM 335
61 DAPPPAPSPFROVSCIKELVAVLQRLCBGAKNTLAFGALLDGAAGCPBAFTTSVR 120
336 DAPPPAPSPFROVSCIKELVAVLQRLCBGAKNTLAFGALLDGAAGCPBAFTTSVR 395
121 SYLNTVTDLRGSGAMGLLRVGDVVLHLARCALFVLVAPSCAYVCCPPLVQLGA 180
396 SYLNTVTDLRGSGAMGLLRVGDVVLHLARCALFVLVAPSCAYVCCPPLVQLGA 455
181 ATQARPPHAGPGRRLGGERAMNHSVREAGVPLGAPGARRRGSSASRSILPLPRPR 240
456 ATQARPPHAGPGRRLGGERAMNHSVREAGVPLGAPGARRRGSSASRSILPLPRPR 515
241 GAAPPEPRTVGGGSAHNGRTGPGSDRGCVVSPARPAEATSLGALSGRHSHPSVG 300
516 GAAPPEPRTVGGGSAHNGRTGPGSDRGCVVSPARPAEATSLGALSGRHSHPSVG 575
301 ROHHAGPSTSRPPRMDTPCPVYAEKFLYSSGDKEQLRPSFLSSLRPSLTGARL 360
576 ROHHAGPSTSRPPRMDTPCPVYAEKFLYSSGDKEQLRPSFLSSLRPSLTGARL 635
361 VETIFLGSPPMGTPRRLPRLPQRYWQMRPLFLEILGNHAQCPYVLLKTCPLRAAT 420
636 VETIFLGSPPMGTPRRLPRLPQRYWQMRPLFLEILGNHAQCPYVLLKTCPLRAAT 695
421 PAAGVCAREKPGSSVAAPEEDTDPRLVQLRGHSSPMQVGYFVACLRILVPPILMGS 480
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481 RHNERFLNTKFKISLGKAKLSLOELTWKMSVBDCAMLRRSPGVGCVPAEHRLEBEI 540
756 RHNERFLNTKFKISLGKAKLSLOELTWKMSVBDCAMLRRSPGVGCVPAEHRLEBEI 815


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0Y 541 LAKFJHMLMSYVYVVELLSFFVETTEQOKNLFYRPSWMSKIOSIGROHKRVORE 600
Db 816 LAKFJHMLMSYVYVVELLSFFVETTEQOKNLFYRPSWMSKIOSIGROHKRVORE 875
0Y 601 LSEAEVRCHREARFALLTSRNFIEKPDGLREIVMDYVVGARTERREKRAERLTSRYKA 660
Db 876 LSEAEVRCHREARFALLTSRNFIEKPDGLREIVMDYVVGARTERREKRAERLTSRYKA 935
0Y 661 LFSVINYRABARRPGLLGASVJGLDIDHABMRFFVLRYAABOPPEPLXYKVDYGAYDTI 720
Db 936 LFSVINYRABARRPGLLGASVJGLDIDHABMRFFVLRYAABOPPEPLXYKVDYGAYDTI 995
0Y 721 PODRLTEVIASIIKEPONTYCVRRYAVVOXAAAGHYRKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 996 PODRLTEVIASIIKEPONTYCVRRYAVVOXAAAGHYRKAFKSHVSTLTDLOPYMRQFVAHL 1055
0Y 781 OETSLRPAVAVIEGSSSLNEASSGFLDYFLRPMCHAVRIRKSYVVOCGIPGSIISTL 840
Db 1056 OETSLRPAVAVIEGSSSLNEASSGFLDYFLRPMCHAVRIRKSYVVOCGIPGSIISTL 1115
0Y 841 LCSLICYGMENKLFAGIRRDGJLLRYVDDFLVTEPHLTHAKTFLRTLVRGYPEYCVNVL 900
Db 1116 LCSLICYGMENKLFAGIRRDGJLLRYVDDFLVTEPHLTHAKTFLRTLVRGYPEYCVNVL 1175
0Y 901 RKTIVNFEVEDEALGCIAPVOMPAHGLFPWCGLLDTRTLEVOSSYSSYARTSRASVTF 960
Db 1176 RKTIVNFEVEDEALGCIAPVOMPAHGLFPWCGLLDTRTLEVOSSYSSYARTSRASVTF 1235
0Y 961 NRGFAGNMRKJLGVRLKXHSJFLDLOVNSLOTCNTNYKILLDQAFEPHACVOLDP 1020
Db 1236 NRGFAGNMRKJLGVRLKXHSJFLDLOVNSLOTCNTNYKILLDQAFEPHACVOLDP 1295
0Y 1021 FHOQWKNPTEFELRYISDTASLCVSLKXAKNAGMSLGAKGAGPLPSEAVOMLCHQAFIL 1080
Db 1296 FHOQWKNPTEFELRYISDTASLCVSLKXAKNAGMSLGAKGAGPLPSEAVOMLCHQAFIL 1355
0Y 1081 KLTRRRVTVVPLGSLRTAQTOLSKLPGTTITALEAANPALBDFKTIID 1132
Db 1356 KLTRRRVTVVPLGSLRTAQTOLSKLPGTTITALEAANPALBDFKTIID 1407

RESULT 6
US-10-325-810-628
; Sequence 628, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Inghner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181

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	FILING DATE:	29-SEP-1997
	APPLICATION NUMBER:	US 08/724,643
	FILING DATE:	01-OCT-1996
	APPLICATION NUMBER:	US 08/844,419
	FILING DATE:	18-APR-1997
	APPLICATION NUMBER:	US 08/846,017
	FILING DATE:	25-APR-1997
	APPLICATION NUMBER:	US 08/851,843
	FILING DATE:	06-MAY-1997
	APPLICATION NUMBER:	US 08/854,050
	FILING DATE:	09-MAY-1997
	APPLICATION NUMBER:	US 08/911,312
	FILING DATE:	14-AUG-1997
	APPLICATION NUMBER:	US 08/912,951
	FILING DATE:	14-AUG-1997
	APPLICATION NUMBER:	US 08/915,503
	FILING DATE:	14-AUG-1997
	APPLICATION NUMBER:	WO PCT/US97/17885
	FILING DATE:	01-OCT-1997
	ATTORNEY/AGENT INFORMATION:	
	NAME:	Ausenhus, Scott L.
	REGISTRATION NUMBER:	42,271
	REFERENCE/DOCKET NUMBER:	015389-002620US
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE:	(415) 576-0200
	TELEFAX:	(415) 576-0300
	SEQUENCE CHARACTERISTICS:	
	LENGTH:	1407 amino acids
	TYPE:	amino acid
	STRANDEDNESS:	<Unknown>
	TOPOLOGY:	linear
	MOLECULE TYPE:	protein
	FEATURE:	
	NAME/KEY:	Protein
	LOCATION:	1..1407
	OTHER INFORMATION:	/note= "fusion protein composed of enhanced green fluorescent protein (EGFP) residues, residues encoded by the 5' untranslated region of hTfR mRNA and hTfR protein sequence"
	SEQUENCE DESCRIPTION:	SEQ ID NO: 628
	US-10-325-810-628	
	Query Match	100.0%; Score 5963; DB 14; Length 1407;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 1132; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
DQ		
DQ	1	MPPAARAVASLLRSYREVLPLATVRRIGPGQWRLVGRGDPAAPALVAQCICVPW 60
DQ	276	MPPAARAVASLLRSYREVLPATVRRIGPGQWRLVGRGDPAAPALVAQCICVPW 335
DQ	61	DARPAPAFSRQYSCKELVARVLQRLCERGANVLAFGFALLDGAGSGPEAFTTSVR 120
DQ	336	DARPAPAFSRQYSCKELVARVLQRLCERGANVLAFGFALLDGAGSGPEAFTTSVR 395
DQ	121	SYLENYTTDLARGGANGLLIRRGDYLVTLLARCAFLVVAFSCAVQVGPFYIYGA 180
DQ	396	SYLENYTTDLARGGANGLLIRRGDYLVTLLARCAFLVVAFSCAVQVGPFYIYGA 455
DQ	181	ATQARPPPHASGPARRLGCERAMNHSVEAGVPLGLPAPGARRRGSASRLPLPKPRR 240
DQ	456	ATQARPPPHASGPARRLGCERAMNHSVEAGVPLGLPAPGARRRGSASRLPLPKPRR 515
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DQ	301	RQHAGGPSTSRPMPDTCCPPYVATFKHLYSSGDKELRPSEGLFSLSPSLTGARL 360
DQ	576	RQHAGGPSTSRPMPDTCCPPYVATFKHLYSSGDKELRPSEGLFSLSPSLTGARL 635
DQ	361	VETIFLSRPMWGTPRRLLPQLQRYWMQRLFTLELLGNHAQCPYGVIILKTHCPRAAVT 420

Db 636 VETIFLGRPMWPGTFRRLPLPQRYWQRPFLTELGHNAOCPPYGVLLKHCPLRAAVT 695
Qy 421 PAAGVARRKPOGSVAPEEDTDPRLTQQLROHSSPMQYGFACRPLVPGMLGS 480
Db 696 PAAGVARRKPOGSVAPEEDTDPRLTQQLROHSSPMQYGFACRPLVPGMLGS 755
Qy 481 RHNERFLNNTKFFISLGHAKLSLOELTWKNSVDCAMLRSPGVGCVPAEHRREI 540
Db 756 RHNERFLNNTKFFISLGHAKLSLOELTWKNSVDCAMLRSPGVGCVPAEHRREI 815
Qy 541 LKPELHMVSVVVELLSPEFYVETTPQKNLFFYRPSVSKLSIGIRHKLXVQRE 600
Db 816 LKPELHMVSVVVELLSPEFYVETTPQKNLFFYRPSVSKLSIGIRHKLXVQRE 875
Qy 601 LSEAEVQRREARPAALLTSRLRFIPKPDGLRPVMDVYVGARTFRREKRAERLTRYKA 660
Db 876 LSEAEVQRREARPAALLTSRLRFIPKPDGLRPVMDVYVGARTFRREKRAERLTRYKA 935
Qy 661 LRSVLNREARRPGLIGASVGLDIDHRAKRTFVLRVAAQDPPELFPYKVDYTAAYTI 720
Db 936 LRSVLNREARRPGLIGASVGLDIDHRAKRTFVLRVAAQDPPELFPYKVDYTAAYTI 995
Qy 721 POPRLTEVASIIRKPONTYCVRRYAVVYKAAHGHYKAFKSHVSTLTLDQPYMRQFVHL 780
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Qy 781 QETSPILDAVVIQSSSLNEASSGLFDVFLRMCHAVIRKGSVYCCGIPQSGILSTL 840
Db 1056 QETSPILDAVVIQSSSLNEASSGLFDVFLRMCHAVIRKGSVYCCGIPQSGILSTL 1115
Qy 841 LCSICGDMENKLFAGIRRDGLLLRVDFELVTPHLTAKTEFLTLVNGVEYECVNL 900
Db 1116 LCSICGDMENKLFAGIRRDGLLLRVDFELVTPHLTAKTEFLTLVNGVEYECVNL 1175
Qy 901 RKTVPNPEDEALGTAIVQVMPAGLFPWCGLLDRTLEVOYSSYARTSIRASYTF 960
Db 1176 RKTVPNPEDEALGTAIVQVMPAGLFPWCGLLDRTLEVOYSSYARTSIRASYTF 1235
Qy 961 NRGFKAGRMRRKLPBGVRLKCHSLFLDQVNSLQVTCNITKILLQAYRHAQVLDLP 1020
Db 1236 NRGFKAGRMRRKLPBGVRLKCHSLFLDQVNSLQVTCNITKILLQAYRHAQVLDLP 1295
Qy 1021 FHQGVKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKAGAPLPSEAVQWLCHQAFLL 1080
Db 1296 FHQGVKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKAGAPLPSEAVQWLCHQAFLL 1355
Qy 1081 KLTRHVVTVPLIGSLRTAQTOLSRKLPETTITALEAANPALBDFKTIID 1132
Db 1356 KLTRHVVTVPLIGSLRTAQTOLSRKLPETTITALEAANPALBDFKTIID 1407

RESULT 7
US-10-877-124-628
Sequence 628, Application US/10877124
Publication No. US20040242529A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Linsner, Joachim
Nakamura, Toru
Chapman, Karen B.
Martin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,124
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 35,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 628:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1407
OTHER INFORMATION: /note= "fusion protein composed of enhanced green fluorescent protein (EGFP) residues, residues encoded by the 5' untranslated region of hTERT mRNA and hTERT protein sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 628:
US-10-877-124-628
Query Match 100.0%; Score 5963; DB 17; Length 1407;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCAVRSLRSLRSHYRVLPLATFVRRLGQGRVTVQRGDPAFRALVQCLVCVM 60
Db 276 MPRAPRCAVRSLRSHYRVLPLATFVRRLGQGRVTVQRGDPAFRALVQCLVCVM 335
Qy 61 DARPAPAPSFROVSCIKELVAVRLQRLGKAGNVLAFGFALLDGAAGGPEPAFTTSVR 120
Db 336 DARPAPAPSFROVSCIKELVAVRLQRLGKAGNVLAFGFALLDGAAGGPEPAFTTSVR 395
Qy 121 SYLPNTYTDLRSGGAGLLIRVGDVTVHLARCALFVIVAPSCAYVCGPPLVQLA 180
Db 396 SYLPNTYTDLRSGGAGLLIRVGDVTVHLARCALFVIVAPSCAYVCGPPLVQLA 455

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QY 181 ATOARPPPHASGPRRLGCEAAMNHSYBAGVPLG:PAPGARRGGASASRLPLPKRPR 240
DB 456 ATOARPPPHASGPRRLGCEAAMNHSYBAGVPLG:PAPGARRGGASASRLPLPKRPR 515
QY 241 GAAPERPTVGGOSMAHPGRTGSDRGFCVVSAPAPAEATSLGASGTEHSHPSVG 300
DB 516 GAAPERPTVGGOSMAHPGRTGSDRGFCVVSAPAPAEATSLGASGTEHSHPSVG 575
QY 301 ROHAGGPTSPRPPMDTCCPPVYATKHFVSSGDKQLRPSFLISSRPSLTARSL 360
DB 576 ROHAGGPTSPRPPMDTCCPPVYATKHFVSSGDKQLRPSFLISSRPSLTARSL 635
QY 361 VETIFLGSPPMGPTRPLRLPQRYWQMRPLFLELLGNHACQPYGLLKTGCPRLAAVT 420
DB 636 VETIFLGSPPMGPTRPLRLPQRYWQMRPLFLELLGNHACQPYGLLKTGCPRLAAVT 695
QY 421 PAAGVCARXKQGSVAAPBEEDTDPRLVOLLKROHSPWQVYGFVACLRILVPPGLMS 480
DB 696 PAAGVCARXKQGSVAAPBEEDTDPRLVOLLKROHSPWQVYGFVACLRILVPPGLMS 755
QY 481 RHNRRLRLTKKFIISLGKAKLSLOELTWMSVDCAMLRSPGVGCVPAAHRRLREEL 540
DB 756 RHNRRLRLTKKFIISLGKAKLSLOELTWMSVDCAMLRSPGVGCVPAAHRRLREEL 815
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DB 876 LSEAEVQOHEARFALLTSRLRFPRDGLRPIVNMVYVGCARTFRREKAEHLTSRVYA 935
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DB 936 LFSVLANERARRPGLIGASYLGLDDIHRAMTFVLRYAODPPEELFYFVADVTAAYDI 995
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DB 1056 QETSPLDVAVIEOSSSLNBSASGLFVFLRFPMCHHARIRGKSYVCCQIGPGSILSTL 1115
QY 841 LCSTCYGDMENKLPAGIRDDGLRLVDDPLVTPHILTHAKTELRLVRGVPYEGCVNL 900
DB 1116 LCSTCYGDMENKLPAGIRDDGLRLVDDPLVTPHILTHAKTELRLVRGVPYEGCVNL 1175
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DB 1176 RKTVMNPFVDEALGTAFAVQMPAHGLFPWCGILLDTRELVOSDVSYSARTSIRASVTF 1235
QY 961 NRGFKAGRMNRKLFVGLRLKCHSLFDLDLVNSLQVTCINIKYLLQAYRFAVYOLP 1020
DB 1236 NRGFKAGRMNRKLFVGLRLKCHSLFDLDLVNSLQVTCINIKYLLQAYRFAVYOLP 1295
QY 1021 FHQGVWKNPFFFLAVISDTASLCSILKANAAGMSLGAKAAGPILBEAOWLCHOAFLL 1080
DB 1296 FHQGVWKNPFFFLAVISDTASLCSILKANAAGMSLGAKAAGPILBEAOWLCHOAFLL 1355
QY 1081 KLTFHRATVYPLGLSLRTAQTOLSRKLPGLTTLTLEAANPALPSDFKTLID 1132
DB 1356 KLTFHRATVYPLGLSLRTAQTOLSRKLPGLTTLTLEAANPALPSDFKTLID 1407

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RESULT 8
US-10-877-022-628
; Sequence 628; Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
;   APPLICANT: Cech, Thomas R.
;   Languer, Joachim
;   Nakamura, Toru

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; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,022
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 03-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 628:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1407 amino acids
; TYPE: amino acid
; STRANDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1407
; OTHER INFORMATION: /note="fusion protein composed of
; enhanced green fluorescent protein
; (EGFP) residues, residues encoded by the
; 5' untranslated region of hTERT mRNA and
; hTERT protein sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 628:
US-10-877-022-628

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Query Match 100.0%; Score 5963; DB 17; Length 1407;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 276 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLGPGGRLVQRGDPAPAFRLVAQCLVCVPM 335
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 DB 336 DAPPAPASFRVYSCLELVARVLQRLCERGAKNVLAFFALLDAGRGPEAFTTSVR 395
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 QY 181 ATQAPPPHSGRRRLGGERAMNHSVREAGVPLGPAFAGARRGGSASRSLPLKRRR 240
 DB 456 ATQAPPPHSGRRRLGGERAMNHSVREAGVPLGPAFAGARRGGSASRSLPLKRRR 515
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 DB 876 LSEAEVQRQREARPALTLRLRPIPKDGLRPIVNMDDYVVGARTRRERARBLRSRYKA 935
 QY 936 LFSVLTYERARRBGLIGASVLGLDIDHRAWTFVLRQAQDPPPELYFKVDVTGAYDTI 995
 DB 661 LFSVLTYERARRBGLIGASVLGLDIDHRAWTFVLRQAQDPPPELYFKVDVTGAYDTI 720
 QY 721 PODRLTEVIASTIKPQNTYCVRRYAVVYCKAAHGRKAFKSHVSTLTDLOPYMRQFVAHL 780
 DB 996 PODRLTEVIASTIKPQNTYCVRRYAVVYCKAAHGRKAFKSHVSTLTDLOPYMRQFVAHL 1055
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 DB 1056 QETSPLRDAVVIQOSSSLNEASSGLFVFLRPMCHAAVARIRKGSYYQCGIPQGSILSTL 1115
 QY 841 LGSICGDMENKLFAGIRRDGILLRLVDDFLVTFHLTHAKTFLATLYRGVPEYCYVNL 900
 DB 1116 LGSICGDMENKLFAGIRRDGILLRLVDDFLVTFHLTHAKTFLATLYRGVPEYCYVNL 1175
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 DB 1236 NGGFAKGRNMRKLFQVLRKCHSLFLDLQVNSLOTVCTNIXKILLQAYRPHACVLOLP 1295
 QY 1021 FHOQWKNQTFPLRVLSDTASLCYSILKXNAGMSLGAAGAAGPLPSEAVOMLGHQAATL 1080
 DB 1296 FHOQWKNQTFPLRVLSDTASLCYSILKXNAGMSLGAAGAAGPLPSEAVOMLGHQAATL 1355

QY 1081 KLTHRYTVYPLLGSJLTAQOTLSRKLPGTTLTALAEANPALPSDFKTLTD 1132
 DB 1356 KLTHRYTVYPLLGSJLTAQOTLSRKLPGTTLTALAEANPALPSDFKTLTD 1407

RESULT 9
 US-09-990-080-2
 ; Sequence 2, Application US/09990080
 ; Patent No. US20020102686A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Genon Corporation
 ; TITLE OF INVENTION: Human telomerase Catalytic Subunit Variants
 ; FILE REFERENCE: 018/258c
 ; CURRENT APPLICATION NUMBER: US/09/990,080
 ; PRIOR FILING DATE: 1998-08-03
 ; PRIOR APPLICATION NUMBER: US 09/052,864
 ; PRIOR FILING DATE: 1998-03-31
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1132
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-990-080-2

Query Match 99.8%; Score 5952; DB 9; Length 1132;
 Best Local Similarity 99.8%; Pred. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLGPGGRLVQRGDPAPAFRLVAQCLVCVPM 60
 DB 1 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLGPGGRLVQRGDPAPAFRLVAQCLVCVPM 60
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 DB 121 SYLNTVTDALRGSGMWGLLRVGDVLYHLARALFVLAAPCAVYCCPPLYOIGA 180
 QY 121 SYLNTVTDALRGSGMWGLLRVGDVLYHLARALFVLAAPCAVYCCPPLYOIGA 180
 DB 121 SYLNTVTDALRGSGMWGLLRVGDVLYHLARALFVLAAPCAVYCCPPLYOIGA 180
 QY 181 ATQAPPPHSGRRRLGGERAMNHSVREAGVPLGPAFAGARRGGSASRSLPLKRRR 240
 DB 181 ATQAPPPHSGRRRLGGERAMNHSVREAGVPLGPAFAGARRGGSASRSLPLKRRR 240
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 DB 241 GAAPBEERTPVGGSWAHFQRTGPDRCFCVSPAPAPAEATSLGALSGTRHSHPSVG 300
 QY 301 ROHHAGPSTSRPPRMDTCCPPVVAETGHLFYSQDKEQLRPSFLSLSLRSLTGARRL 360
 DB 301 ROHHAGPSTSRPPRMDTCCPPVVAETGHLFYSQDKEQLRPSFLSLSLRSLTGARRL 360
 QY 361 VETIFLGSRPMMGTERRRLPLRQRYWQMRPLFLELLGNHAQCPYGLLKTCHPLRAAVT 420
 DB 361 VETIFLGSRPMMGTERRRLPLRQRYWQMRPLFLELLGNHAQCPYGLLKTCHPLRAAVT 420
 QY 421 PAAGVCAAREKPOGSVAABEEDTDPRRLVOLLROHSSPMQYGVFRACLRLVPPGLMGS 480
 DB 421 PAAGVCAAREKPOGSVAABEEDTDPRRLVOLLROHSSPMQYGVFRACLRLVPPGLMGS 480
 QY 481 RHNERFRLNTKKFISLGHAKLSLOELTWKMSVBCAALRRSPGVGCPAPAEHRLREI 540
 DB 481 RHNERFRLNTKKFISLGHAKLSLOELTWKMSVBCAALRRSPGVGCPAPAEHRLREI 540
 QY 541 LAKFLHMLSVYVVELLRSEFFVYETTFQKNLFFYRPSVMSKLSIGIRQHLKRYQURE 600
 DB 541 LAKFLHMLSVYVVELLRSEFFVYETTFQKNLFFYRPSVMSKLSIGIRQHLKRYQURE 600
 QY 601 LSEAEVQRQREARPALTLRLRPIPKDGLRPIVNMDDYVVGARTRRERARBLRSRYKA 660
 DB 601 LSEAEVQRQREARPALTLRLRPIPKDGLRPIVNMDDYVVGARTRRERARBLRSRYKA 660

QY 661 LFSVLYNERARRPGLGASVGLDDIHRAMRTFVLRAADPPPELYFVKVDTGAYDTI 720
DB 661 LFSVLYNERARRPGLGASVGLDDIHRAMRTFVLRAADPPPELYFVKVDTGAYDTI 720
QY 721 PODRLTEVIASIIKQNTYCVARYAVVQKAHGHVRAFKSHVSTLTDLOPYMRQFVAHL 780
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DB 781 QETSPLRDVAVIEOSSSINBASGLFDVFLRPMCHAVIRIGKSVYOCQIGIPQGSIIISTL 840
QY 841 LCSLCYGMENKLFAGIRRDGILLRLVDDFLVTPHILTHAKTFLRTLVRCVPEXCVVNL 900
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QY 901 RKTIVNFPVEDEALGCTAFVQMPAHGLFPMCGILDLTRLEVOSSYARTSIRASLTF 960
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QY 1021 FHQVWKNPFFFLRISDTASLCSYLKANNAGMSLGAKGAGLPSEAVQWMLCHQAFLL 1080
DB 1021 FHQVWKNPFFFLRISDTASLCSYLKANNAGMSLGAKGAGLPSEAVQWMLCHQAFLL 1080
QY 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPQTTLTLTAANPALPSPDKTILLD 1132
DB 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPQTTLTLTAANPALPSPDKTILLD 1132

RESULT 10

US-09-749-728B-31
; Sequence 31, Application US/09749728B
; Patent No. US2020142457A1
; GENERAL INFORMATION:
; APPLICANT: Umezawa, Akihiro
; APPLICANT: Hata, Jun-ichi
; APPLICANT: Fukuda, Keiichi
; APPLICANT: Ogawa, Satoshi
; APPLICANT: Sakurada, Kazuhiko
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMY
; FILE REFERENCE: 06766.00043
; CURRENT APPLICATION NUMBER: US/09/749, 728B
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: H11-372826
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: PCT-JP00-01148
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT-JP00-07741
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 31
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-749-728B-31

Query Match 99.8%; Score 5952; DB 9; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAAPCRAYSLRSHRYEVLPLATFVRRLPGQWMLVORGPAARALVACLVCPV 60
DB 1 MPRAAPCRAYSLRSHRYEVLPLATFVRRLPGQWMLVORGPAARALVACLVCPV 60
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DB 61 DARPPPAAPSPFQVSCLEKELVAVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
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DB 121 SYLPNTVTDALFGSGAMGILLRRVGDVYLHILARCALPVLVAPCAVQCCPELYOJCA 180
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DB 301 RQHHAGPSTSRPPPMWTPCPBPVYAEIKHFLYSSGDKEQLRPSFLSLRPSLIGARRL 360
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DB 361 VETIFLGSHPWMPGTPRRLPRLPQRYWQMRPFLELGNHAQCPYGVLLKTHCPLRAAVT 420
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DB 421 PAAGVCANRKPQGSVAAEBEEDTDRRLVOLLRQSSFWOYGFRACLRLVPPGMLGS 480
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DB 481 RENERRFLRNTKFFSLGKHAFLSLOELTWKSVYDCAMLRSPVGVCAPEAHEHREI 540
QY 541 IAKFLHMLMSVYVVELLSFFVYETTFQKRLFFYRPSVMSKIOSIGIRHLKAVQURE 600
DB 541 IAKFLHMLMSVYVVELLSFFVYETTFQKRLFFYRPSVMSKIOSIGIRHLKAVQURE 600
QY 601 LSEAEVROHREARPLTLRSRLFTPKPDLRPIVMDVYVAGARTREKREARLRSRKA 660
DB 601 LSEAEVROHREARPLTLRSRLFTPKPDLRPIVMDVYVAGARTREKREARLRSRKA 660
QY 661 LFSVLYNERARRPGLGASVGLDDIHRAMRTFVLRAADPPPELYFVKVDTGAYDTI 720
DB 661 LFSVLYNERARRPGLGASVGLDDIHRAMRTFVLRAADPPPELYFVKVDTGAYDTI 720
QY 721 PODRLTEVIASIIKQNTYCVARYAVVQKAHGHVRAFKSHVSTLTDLOPYMRQFVAHL 780
DB 721 PODRLTEVIASIIKQNTYCVARYAVVQKAHGHVRAFKSHVSTLTDLOPYMRQFVAHL 780
QY 781 QETSPLRDVAVIEOSSSINBASGLFDVFLRPMCHAVIRIGKSVYOCQIGIPQGSIIISTL 840
DB 781 QETSPLRDVAVIEOSSSINBASGLFDVFLRPMCHAVIRIGKSVYOCQIGIPQGSIIISTL 840
QY 841 LCSLCYGMENKLFAGIRRDGILLRLVDDFLVTPHILTHAKTFLRTLVRCVPEXCVVNL 900
DB 841 LCSLCYGMENKLFAGIRRDGILLRLVDDFLVTPHILTHAKTFLRTLVRCVPEXCVVNL 900
QY 901 RKTIVNFPVEDEALGCTAFVQMPAHGLFPMCGILDLTRLEVOSSYARTSIRASLTF 960
DB 901 RKTIVNFPVEDEALGCTAFVQMPAHGLFPMCGILDLTRLEVOSSYARTSIRASLTF 960
QY 961 NRGFKARNRMRKLFVLRKCHSLFDLOVNSIQVCTNIYKILLQAFRFAVLOLP 1020
DB 961 NRGFKARNRMRKLFVLRKCHSLFDLOVNSIQVCTNIYKILLQAFRFAVLOLP 1020
QY 1021 FHQVWKNPFFFLRISDTASLCSYLKANNAGMSLGAKGAGLPSEAVQWMLCHQAFLL 1080
DB 1021 FHQVWKNPFFFLRISDTASLCSYLKANNAGMSLGAKGAGLPSEAVQWMLCHQAFLL 1080
QY 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPQTTLTLTAANPALPSPDKTILLD 1132
DB 1081 KLTRHRTVYVPLGSLRTAQTOLSRKLPQTTLTLTAANPALPSPDKTILLD 1132

RESULT 11

US-09-843-676-225
 ; Sequence 225, Application US/09843676
 ; Patent No. US20020164786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cecch, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Hatley, Calvin B.
 ; Andrews, William H.
 ; TITLE OF INVENTION: No. US20020164786A1e1 Telomerase
 ; NUMBER OF SEQUENCES: 225
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/843,676
 ; FILING DATE: 26-Apr-2001
 ; CLASSIFICATION: 535
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/854,050
 ; FILING DATE: 09-May-1997
 ; APPLICATION NUMBER: US/08/846,017
 ; FILING DATE: 25-Apr-1997
 ; APPLICATION NUMBER: US/08/844,419
 ; FILING DATE: 18-Apr-1997
 ; APPLICATION NUMBER: US/08/724,643
 ; FILING DATE: 01-Oct-1996
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 015389-002930US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ;
 ; INFORMATION FOR SEQ ID NO: 225:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1132 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 225:
 ;
 ; US-09-843-676-225
 ;
 ; Query Match 99.8%; Score 5952; DB 9; Length 1132;
 ; Best Local Similarity 99.8%; Pred. No. 0;
 ; Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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 ; Db 1 MRPAPPCRAVRSILRSHYREVLPPLATFVRRLGPOGMRVQRGDPAPAFALVAQCVCVPM 60
 ; QY 1 MRPAPPCRAVRSILRSHYREVLPPLATFVRRLGPOGMRVQRGDPAPAFALVAQCVCVPM 60
 ; Db 61 DARPPPAASFRQVSCLEKELVARVLORLCERGAQVLAFFALDGAAGPPEAATTSVR 120
 ; QY 61 DARPPPAASFRQVSCLEKELVARVLORLCERGAQVLAFFALDGAAGPPEAATTSVR 120
 ; Db 121 SYLPNTVTDLRSGAGMLLRVGDVVLVLLARCALFVLVAPSCAVQVCGPPLVQIGA 180
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 ; QY 121 SYLPNTVTDLRSGAGMLLRVGDVVLVLLARCALFVLVAPSCAVQVCGPPLVQIGA 180
 ; Db 181 ATQARPPPAASGRRLGCEERAMNHSVPRAGVPLGIPAPGARRRGSAASRLPLPKRRR 240
 ; QY 181 ATQARPPPAASGRRLGCEERAMNHSVPRAGVPLGIPAPGARRRGSAASRLPLPKRRR 240
 ; Db 181 ATQARPPPAASGRRLGCEERAMNHSVPRAGVPLGIPAPGARRRGSAASRLPLPKRRR 240
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QY 241 GAAPERTPTVGGGSNAHPGRTGRGDRGCVVSPAPAPBEATSLGALSGTRHSPSYG 300
 Db 241 GAAPERTPTVGGGSNAHPGRTGRGDRGCVVSPAPAPBEATSLGALSGTRHSPSYG 300
 QY 301 ROHHAGPPSTSRPPRPMDTPCPVVAETKHFVLSGDXEQLRPSFLLSSLRBSLTGARL 360
 Db 301 ROHHAGPPSTSRPPRPMDTPCPVVAETKHFVLSGDXEQLRPSFLLSSLRBSLTGARL 360
 QY 361 VETIFLGSRRPMPGTPRLRLPQRYQMPPLLELLGNHACQCVVLKTHCPLEAAVT 420
 Db 361 VETIFLGSRRPMPGTPRLRLPQRYQMPPLLELLGNHACQCVVLKTHCPLEAAVT 420
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 Db 421 PAAGVCAERKQPSVAAPBEEDTDPRRLVQLLRQHSPPQVYGFVACURLVPPLMG 480
 QY 481 RHNERRLRNTKCFISLGKAKLSIDELTWKNSVRCALRLRSPGVGCVAEHRLEET 540
 Db 481 RHNERRLRNTKCFISLGKAKLSIDELTWKNSVRCALRLRSPGVGCVAEHRLEET 540
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 Db 541 LAKFLHWSVYVVELRSFFVYTTETFOKNRLFYRPSWSKLSIGIRHLKRYQLE 600
 QY 601 LSAEVRQHRKAPALITSLRPIPKPDGIRPIVMDYVGAFTFRERGAERLISRYKA 660
 Db 601 LSAEVRQHRKAPALITSLRPIPKPDGIRPIVMDYVGAFTFRERGAERLISRYKA 660
 QY 661 LFSVLYNERARRPGLIGASVLAGDDIHRAMRTVLVRAODPEPELYFKVDVTGAYDTI 720
 Db 661 LFSVLYNERARRPGLIGASVLAGDDIHRAMRTVLVRAODPEPELYFKVDVTGAYDTI 720
 QY 721 PODRLTEVIASIIKPOVTYCVRRYAVVOXAAHGHVAKFSHVSTLTDLQPYMRQFAHL 780
 Db 721 PODRLTEVIASIIKPOVTYCVRRYAVVOXAAHGHVAKFSHVSTLTDLQPYMRQFAHL 780
 QY 781 QETSPLEDAVITQSSSLNENASGLDVLRFVCHNAVIRGKSVYQCGGIGOGSLSTL 840
 Db 781 QETSPLEDAVITQSSSLNENASGLDVLRFVCHNAVIRGKSVYQCGGIGOGSLSTL 840
 QY 841 LGSICYGDMENKLFAGIRRDGLLRVDDPLVTPHLLHAKFRLTLVGEVEYGCVM 900
 Db 841 LGSICYGDMENKLFAGIRRDGLLRVDDPLVTPHLLHAKFRLTLVGEVEYGCVM 900
 QY 901 RKTIVNFPVEDALGTAFTQMPAHGLFPGCGILLDRLEVOSSVSAFRTSIRASLT 960
 Db 901 RKTIVNFPVEDALGTAFTQMPAHGLFPGCGILLDRLEVOSSVSAFRTSIRASLT 960
 QY 961 NRGFKAGNNRKLFGVLRKCHSLFLDLQVNSLQVCTNIYKILLQAYRPAVCYLQ 1020
 Db 961 NRGFKAGNNRKLFGVLRKCHSLFLDLQVNSLQVCTNIYKILLQAYRPAVCYLQ 1020
 QY 1021 FHQVWKNPTFLRLVISTASLCYSILKAKNAGMSIGAKGAGPLPSEAVQMLCHQAPLL 1080
 Db 1021 FHQVWKNPTFLRLVISTASLCYSILKAKNAGMSIGAKGAGPLPSEAVQMLCHQAPLL 1080
 QY 1081 KLTRHRVTYVPLIGSLRTAQTLRGLPGLTTLTALPAAANPALPSPFKILLD 1132
 Db 1081 KLTRHRVTYVPLIGSLRTAQTLRGLPGLTTLTALPAAANPALPSPFKILLD 1132
 ;
 ; RESULT 12
 ; US-09-953-052-2
 ; Sequence 2, Application US/09953052
 ; Patent No. US20020173476A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cecch, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Hatley, Calvin B.

Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,052
FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2
Query Match 99.8%; Score 5952; DB 9; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

121 SYLPTVTDALRGSGMGLLRVGDVTLVHLARCALFVLVAPSCAYQVGGPPLYQGA 180
121 SLTPNTVTDALRGSGMGLLRVGDVTLVHLARCALFVLVAPSCAYQVGGPPLYQGA 180
181 ATQAPPFHASGPRRRRLCERAMNHSVAEAGVPLGLPAPGARRRGASASRLPLKRRR 240
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541 LAKFLHMLMSYVVVLLASFFVYVETTFQKRLPFYRSVSKOSIGIRQHLKRYQRE 600
541 LAKFLHMLMSYVVVLLASFFVYVETTFQKRLPFYRSVSKOSIGIRQHLKRYQRE 600
601 LSEAERQHRERAPLTLTSRLFLIPKPDGLRPIVMQDVYARTFRERREKAEZRLTSRYKA 660
601 LSEAERQHRERAPLTLTSRLFLIPKPDGLRPIVMQDVYARTFRERREKAEZRLTSRYKA 660
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841 LCSLCYGMENKLPFGIRRDGLLELVNDEPLLVPHLTHAKTFLRTVIRGPEGVGNL 900
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901 RKTVPNPFVEDEALGGLTAFVQMPAHGLFPWCGLLDITLTLEQSDYSSYARTSIRASYTF 960
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961 NRGFAGGRMRKLFGLVRLKCHSLFDLVQNSLQTVNTYKILLQAYRFAHCVQLP 1020
1021 FHQGVKQKPTFLRLVISTYASLCYILAKKAGMSLGAKGAGPLPSBAVQMLCHQAFLL 1080
1021 FHQGVKQKPTFLRLVISTYASLCYILAKKAGMSLGAKGAGPLPSBAVQMLCHQAFLL 1080
1081 KLTRHRTVYVPLGSLRTAQQLSRKLPGLTTLALEAANPALPSDFETIID 1132
1081 KLTRHRTVYVPLGSLRTAQQLSRKLPGLTTLALEAANPALPSDFETIID 1132
RESULT 13
US-09-788-110A-23
; Sequence 23, Application US/09788110A
; Publication No. US20040086518A1


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; GENERAL INFORMATION:
; APPLICANT: Zanetti, Maurizio
; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing
; TITLE OF INVENTION: Telomerase Reverse Transcriptase
; FILE REFERENCE: UCSD-07017
; CURRENT APPLICATION NUMBER: US/09/788,110A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-788-110A-23

Query Match          99.8%; Score 5952; DB 11; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRLSHREYVPLATFVRRLGPQGRVLRQGDPAAFRLVAQCLVCVPM 60
DB 1 MPAPRCRAVRLSHREYVPLATFVRRLGPQGRVLRQGDPAAFRLVAQCLVCVPM 60
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DB 61 DAPPPAASPFRQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGPPEAFTTSVR 120
QY 121 SYLNTVTDTALRGSGAGLLLRVGDVVLHLLARCALFVLVASCAYQCGPPIYQGA 180
DB 121 SYLNTVTDTALRGSGAGLLLRVGDVVLHLLARCALFVLVASCAYQCGPPIYQGA 180
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DB 181 ATGAPRPPASGRRRLGGERAMNSVREAGVPLGLPAPGARRGSSASRSLPLPKRRR 240
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QY 361 VETIFGSRPMWPGTFRLLPRLPORYQWRPFLLELLGNHACPPYVLLKTHCPRLAAVT 420
DB 361 VETIFGSRPMWPGTFRLLPRLPORYQWRPFLLELLGNHACPPYVLLKTHCPRLAAVT 420
QY 421 PAAGVCAAREKPOGSVAAPBEDTDRRLVOLLROHSSPWQYGFYRACLRRLVPPGLMGS 480
DB 421 PAAGVCAAREKPOGSVAAPBEDTDRRLVOLLROHSSPWQYGFYRACLRRLVPPGLMGS 480
QY 481 RNNRRFLNTKKEFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHLRSEI 540
DB 481 RNNRRFLNTKKEFISLGHAKLSLOELTWKMSVDCAMLRSPGVGCVPAAEHLRSEI 540
QY 541 LAKFLHMLMSVYVELLSFFVYVETTFQKRLFFYRPSVSKLOSIGIRQHLKRVQURE 600
DB 541 LAKFLHMLMSVYVELLSFFVYVETTFQKRLFFYRPSVSKLOSIGIRQHLKRVQURE 600
QY 601 LSEAEVRQREARPAALTSRLRFIPKPDGLRIYMDYVVGARTFRREARERLSRYKA 660
DB 601 LSEAEVRQREARPAALTSRLRFIPKPDGLRIYMDYVVGARTFRREARERLSRYKA 660
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DB 661 LFSVLYNEARRRPGLIGASVLGLDIDIRAMRTFVLRAQDPPELYVKVDYTGAYDTI 720
QY 721 PODRLTEVIASTIKPONTYCVRRYAVVQCAAGHGRKAFKSVSLTLOPVMRFVHL 780
DB 721 PODRLTEVIASTIKPONTYCVRRYAVVQCAAGHGRKAFKSVSLTLOPVMRFVHL 780
QY 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYQCCGIPQGSILSTL 840

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DB 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYQCCGIPQGSILSTL 840
QY 841 LCSLCYGDMMENKLFAGIRBDLLRLVDDFLVTPALHTAKFRLRLVGVGEYCVNL 900
DB 841 LCSLCYGDMMENKLFAGIRBDLLRLVDDFLVTPALHTAKFRLRLVGVGEYCVNL 900
QY 901 RKTYYNPFVDEALGGAFFQMPAGLFPWCGILLDTFRLEQSDSSYARSISRLTF 960
DB 901 RKTYYNPFVDEALGGAFFQMPAGLFPWCGILLDTFRLEQSDSSYARSISRLTF 960
QY 961 NRGFKAGNRRLKFGVLRKCHSLFLDLQVNSLQTVCTNIVYLLDQAFRAVCLQLP 1020
DB 961 NRGFKAGNRRLKFGVLRKCHSLFLDLQVNSLQTVCTNIVYLLDQAFRAVCLQLP 1020
QY 1021 FHOQVKNPFFLRVISTDASLCYSILKAKNAGMSIGAKGAGPLPSEAVQWICHQAFLL 1080
DB 1021 FHOQVKNPFFLRVISTDASLCYSILKAKNAGMSIGAKGAGPLPSEAVQWICHQAFLL 1080
QY 1081 KLTRHRTVYPLGSLRTAQTOLSRKLPSTTLTALBAANPALPSPDKTILD 1132
DB 1081 KLTRHRTVYPLGSLRTAQTOLSRKLPSTTLTALBAANPALPSPDKTILD 1132

RESULT 14
US-10-053-758-225
; Sequence 225, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
;           Lingner, Joachim
;           Nakamura, Toru
;           Chapman, Karen B.
;           Morin, Gregg B.
;           Harley, Calvin
;           Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 01589-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:

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LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 225:
 US-10-053-758-225

Query Match 99.8%; Score 5952; DB 14; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MPAPRCRAVSLRSHRYREVLPATFVRRLGPOGMRVORGPAPAFALVAQCIVCVPM 60
DB 1 MPAPRCRAVSLRSHRYREVLPATFVRRLGPOGMRVORGPAPAFALVAQCIVCVPM 60
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DB 61 DAPPPAPSPFQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGAAGPPEAFTTSVR 120
QY 121 SYLPTVTDLRSGGAMGLLRVGDVYLHLLARCALFVLVAPSCAYOVCGSPLYQLGA 180
DB 121 SYLPTVTDLRSGGAMGLLRVGDVYLHLLARCALFVLVAPSCAYOVCGSPLYQLGA 180
QY 181 ATQARPPHASPGRRLCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
DB 181 ATQARPPHASPGRRLCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
QY 241 GAAPPERTVVGQGSWAPRGTRGSPDRGFCVSPAPAEATSLGALSCTHSHPSVG 300
DB 241 GAAPPERTVVGQGSWAPRGTRGSPDRGFCVSPAPAEATSLGALSCTHSHPSVG 300
QY 301 ROHHAGPSTSRPRPMDTCPPIVAETKHFVLYSSGDKELRSPFLSLRPSLTGARRL 360
DB 301 ROHHAGPSTSRPRPMDTCPPIVAETKHFVLYSSGDKELRSPFLSLRPSLTGARRL 360
QY 361 VETITLGSRRPMPGTGPRRLPLRPLQRYWQMRPLFLELLGNHAQCPGYVLKTHGCLRAAVT 420
DB 361 VETITLGSRRPMPGTGPRRLPLRPLQRYWQMRPLFLELLGNHAQCPGYVLKTHGCLRAAVT 420
QY 421 PAAGVCAERKPGQSVAAPEEDMDPRLYOLLRQHSPPQVGVPAACRLVLPGLMGS 480
DB 421 PAAGVCAERKPGQSVAAPEEDMDPRLYOLLRQHSPPQVGVPAACRLVLPGLMGS 480
QY 481 RHNERRLRNTKFTSLGKNAKLSLOELTWKMSVRCDAWLRSPGVOCVPAAEHRLREEL 540
DB 481 RHNERRLRNTKFTSLGKNAKLSLOELTWKMSVRCDAWLRSPGVOCVPAAEHRLREEL 540
QY 541 LAKEFLHLMVYVVELLRSFFYTEETFOKORLFFRPSPWSKLOSGITGHOHKRQVLE 600
DB 541 LAKEFLHLMVYVVELLRSFFYTEETFOKORLFFRPSPWSKLOSGITGHOHKRQVLE 600
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DB 601 LSEAEVQHEAPRALLTSRLRFIPKPDGLPIYNDVYVGARTPREKKAEBLTGRVKA 660
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DB 661 LFSVANTERRARRPGLIGASVILGDDIHRAMRTFVLRAADPPPELFEVAVDTGAYDTI 720
QY 721 POBLRTVIAISIKPONTYCVRRYAVYQKAAGHVRKAFKSHVSTLTDLOPYRKQVAHL 780
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QY 781 QETSPLRDVAVYIEGSSSLNASSGLFDVPLRFMCHNAVRIKGSYYVCCQIPGSSILSTL 840
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DB 841 LCSTCYGDMEKULFAGIRROGLILRLVDDFLVTPHILTHAKTLRTLYRVQPEYGCVM 900
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DB 1021 FHQVWKNKPTFRLVISTASTLQVSIILKAKAGMSLGAAGPLPSRAVQWLCHQAFLL 1080
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DB 1081 KLTRHRTVYVPLGSLRTAQTQSLRKLPGTTLTALEAANPALPSPDFKTIID 1132

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RESULT 15
 US-10-208-243-2
 ; Sequence 2, Application US/10208243
 ; Publication No. US20030044394A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaeta, Federico C.A.
 ; APPLICANT: Genon Corporation
 ; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
 ; FILE REFERENCE: 015389-003500PC
 ; CURRENT APPLICATION NUMBER: US/10/208,243
 ; CURRENT FILING DATE: 2002-07-30
 ; PRIOR APPLICATION NUMBER: US/09/675,321
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: US 60/112,006
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
 ; PRIOR FILING DATE: 1999-03-30
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1132
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-208-243-2

Query Match 99.8%; Score 5952; DB 14; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 361 VETITLGSRRPMPGTGPRRLPLRPLQRYWQMRPLFLELLGNHAQCPGYVLKTHGCLRAAVT 420

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-054-295-225

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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D 1 MPAPRCRAVRSILRSHYREVLPATFVRRLGPOGRLVQGDPAAPALVAQCLVCVM 60
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	Query Match	99.8%	Score 5952	DB 14	Length 1132
Matches	Local Similarity	99.8%	Pred. No. 0		
Batch 1130	Conservative	1	Mismatches	1	Indels 0; Gaps 0
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Qy 721 PQRRLTEVASTIKPONTYCVRRYAVVQAAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PQRRLTEVASTIKPONTYCVRRYAVVQAAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAAVIRKGSYVOCGIGIPOGSLSTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAAVIRKGSYVOCGIGIPOGSLSTL 840
Qy 841 LCSLCYGDMEKLFAGIRRDGILLRLVDDPLVTPHLLTHAKTFLRLTVRGVEYGCYVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGILLRLVDDPLVTPHLLTHAKTFLRLTVRGVEYGCYVNL 900
Qy 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPMCGILLDTRTLEVOSSYSAFTSIRASVTF 960
Db 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPMCGILLDTRTLEVOSSYSAFTSIRASVTF 960
Qy 961 NRGFKAGRNRRKLFVGLRLKCHSLFLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
Db 961 NRGFKAGRNRRKLFVGLRLKCHSLFLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
Qy 1021 FHQQVWKNPFFFLRVISDTASLCYSTLKAKNAGMSLGAGAGAPLPSEAVQMLCHQAFLL 1080
Db 1021 FHQQVWKNPFFFLRVISDTASLCYSTLKAKNAGMSLGAGAGAPLPSEAVQMLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLIGSLRTAQOTLSRKLPGTTLTALAAANPALPSDFKTIID 1132
Db 1081 KLTRHRVTYVPLIGSLRTAQOTLSRKLPGTTLTALAAANPALPSDFKTIID 1132

RESULT 18
US-10-105-963-2
; Sequence 2, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Deming, Chris
; APPLICANT: Clark, A. John
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-963-2

Query Match          99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRRAPRCRAVRSILRSHREYV..PLATFVRLGPQGMRLVORGDPAFAFALVAOCIVCPW 60
Db 1 MRRAPRCRAVRSILRSHREYV..PLATFVRLGPQGMRLVORGDPAFAFALVAOCIVCPW 60
Qy 61 DARPPPAASFRQVSCIKELVAVRQRLCERAGKVVLAFGPALLDGAAGGPEAFITTSVR 120
Db 61 DARPPPAASFRQVSCIKELVAVRQRLCERAGKVVLAFGPALLDGAAGGPEAFITTSVR 120
Qy 121 SYLPNTVTDALRGSAGWGLLRVRVDVVLVHLAFCALFVLVAPSCAYQVGPPLYQGA 180
Db 121 SYLPNTVTDALRGSAGWGLLRVRVDVVLVHLAFCALFVLVAPSCAYQVGPPLYQGA 180
Qy 181 ATQARPAPPAASGPRRLGGERAMNHSVNBAGVPLGLPAPGARRRGGASRLPLPKRPRR 240
Db 181 ATQARPAPPAASGPRRLGGERAMNHSVNBAGVPLGLPAPGARRRGGASRLPLPKRPRR 240

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Qy 241 GAAPERTYVQGGSMHAPGRTGSPSDRGFCVVSPPARPAEATSLGALSGTRHSPVSG 300
Db 241 GAAPERTYVQGGSMHAPGRTGSPSDRGFCVVSPPARPAEATSLGALSGTRHSPVSG 300
Qy 301 ROHAGPSTSPRPPMDTFCPPVYAEETKHELVSDDKEQRLRSFTLSLSPSLTARBL 360
Db 301 ROHAGPSTSPRPPMDTFCPPVYAEETKHELVSDDKEQRLRSFTLSLSPSLTARBL 360
Qy 361 VETIFLGSRRPMDGTPRRLPLRLPQRYWQMPFLFLELLGNHAGCPYGVLLKTHCPLEAAVT 420
Db 361 VETIFLGSRRPMDGTPRRLPLRLPQRYWQMPFLFLELLGNHAGCPYGVLLKTHCPLEAAVT 420
Qy 421 PAAGVCAKREKQGSVAAPREEDTPRRVLQVLEQSHSPQVYGFVACLRRLVPELWMS 480
Db 421 PAAGVCAKREKQGSVAAPREEDTPRRVLQVLEQSHSPQVYGFVACLRRLVPELWMS 480
Qy 481 RHNERRLRNTKFFISIGKAKLSLOELTWKMSVRCQAMLRSPGVGCYVPAAEHRLREEI 540
Db 481 RHNERRLRNTKFFISIGKAKLSLOELTWKMSVRCQAMLRSPGVGCYVPAAEHRLREEI 540
Qy 541 LAKFLWMSVYVELLRFFYTETTFQONRLFPRPSVMSKLSIGIRHLKRYOLRE 600
Db 541 LAKFLWMSVYVELLRFFYTETTFQONRLFPRPSVMSKLSIGIRHLKRYOLRE 600
Qy 601 LSEAEVQOHEARAPALTSRLRFIPKPDGLRPIVNMDDYVVGARTPREKRAERLTSRYKA 660
Db 601 LSEAEVQOHEARAPALTSRLRFIPKPDGLRPIVNMDDYVVGARTPREKRAERLTSRYKA 660
Qy 661 LPSVLYNERARPPGLIGASYLGDDIHRAIRFVLRADQPPPELYFVKVVTGAYDTI 720
Db 661 LPSVLYNERARPPGLIGASYLGDDIHRAIRFVLRADQPPPELYFVKVVTGAYDTI 720
Qy 721 PQRRLTEVASTIKPONTYCVRRYAVVQAAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PQRRLTEVASTIKPONTYCVRRYAVVQAAHGHVAKAFKSHVSTLTDLOPYMRQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAAVIRKGSYVOCGIGIPOGSLSTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAAVIRKGSYVOCGIGIPOGSLSTL 840
Qy 841 LCSLCYGDMEKLFAGIRRDGILLRLVDDPLVTPHLLTHAKTFLRLTVRGVEYGCYVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGILLRLVDDPLVTPHLLTHAKTFLRLTVRGVEYGCYVNL 900
Qy 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPMCGILLDTRTLEVOSSYSAFTSIRASVTF 960
Db 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPMCGILLDTRTLEVOSSYSAFTSIRASVTF 960
Qy 961 NRGFKAGRNRRKLFVGLRLKCHSLFLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
Db 961 NRGFKAGRNRRKLFVGLRLKCHSLFLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
Qy 1021 FHQQVWKNPFFFLRVISDTASLCYSTLKAKNAGMSLGAGAGAPLPSEAVQMLCHQAFLL 1080
Db 1021 FHQQVWKNPFFFLRVISDTASLCYSTLKAKNAGMSLGAGAGAPLPSEAVQMLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLIGSLRTAQOTLSRKLPGTTLTALAAANPALPSDFKTIID 1132
Db 1081 KLTRHRVTYVPLIGSLRTAQOTLSRKLPGTTLTALAAANPALPSDFKTIID 1132

RESULT 19
US-10-044-692-2
; Sequence 2, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin

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Tue Dec 21 15:43:31 2004

us-08-974-584c-118.rapb

Page 19

Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-044-692-2
Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1133; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

301 ROHAGPESTSRPPRMDTPCPVYAEKHFYSSGDEQRLPESLSSRLTGARL 360
301 ROHAGPESTSRPPRMDTPCPVYAEKHFYSSGDEQRLPESLSSRLTGARL 360
361 VETIFLGRPMWPGTFRRLPRLPQRYWQMRPLFELLGNHAQCPYGVILKTHCPILRAVT 420
361 VETIFLGRPMWPGTFRRLPRLPQRYWQMRPLFELLGNHAQCPYGVILKTHCPILRAVT 420
421 PAAGCAREKPOGSAVAPEEDTPRRLYOCLRGSSPMQYGFACRLRLVPGELGS 480
421 PAAGCAREKPOGSAVAPEEDTPRRLYOCLRGSSPMQYGFACRLRLVPGELGS 480
481 RHNERFLRNTKFIISLGHAKLSLOELTWKMSYRDCAMLRSPGVGCPAAEHLREEL 540
481 RHNERFLRNTKFIISLGHAKLSLOELTWKMSYRDCAMLRSPGVGCPAAEHLREEL 540
541 LAKFLHMLMSYVYVLLASFYVYTTTFOKNRPLFFRPSVMSKLSIGIRQLKRVQIRE 600
541 LAKFLHMLMSYVYVLLASFYVYTTTFOKNRPLFFRPSVMSKLSIGIRQLKRVQIRE 600
601 LSEAERQHRERARPALTSRLRFLPKPDGLRPIVMDYVGAFTFRERKAEHLTSRYKA 660
601 LSEAERQHRERARPALTSRLRFLPKPDGLRPIVMDYVGAFTFRERKAEHLTSRYKA 660
661 LFSVUNYRARRPGLLGASVUGLDDIHRAMRTFVLRYAQAOPPELRYVKVDVTGAYDTI 720
661 LFSVUNYRARRPGLLGASVUGLDDIHRAMRTFVLRYAQAOPPELRYVKVDVTGAYDTI 720
721 PODRLTEVIASIKPQNTYCYRRAVVOKAAGHVRKAFKSHVSTLTDLOPMRQFVAHL 780
721 PODRLTEVIASIKPQNTYCYRRAVVOKAAGHVRKAFKSHVSTLTDLOPMRQFVAHL 780
761 QETSPDLDAVYIEGSSSINEASSGLFDYFLRFMCHAVRIRKSYVOCQIPQSSILSTL 840
761 QETSPDLDAVYIEGSSSINEASSGLFDYFLRFMCHAVRIRKSYVOCQIPQSSILSTL 840
841 LCLSLCYGMENKLFPGIRRDGLRLVDDFLVPHLTHAKTFLRTLVRGVPEGCYVNL 900
841 LCLSLCYGMENKLFPGIRRDGLRLVDDFLVPHLTHAKTFLRTLVRGVPEGCYVNL 900
901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVOSSYARTSIRASVTF 960
901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVOSSYARTSIRASVTF 960
961 NRGFAGKMRMRKLFQVIRIKCHSIFLDLOVNSIQVCTNITYKILLQAYRPHACVQLP 1020
961 NRGFAGKMRMRKLFQVIRIKCHSIFLDLOVNSIQVCTNITYKILLQAYRPHACVQLP 1020
1021 FHQVWKNPTFFLRISDTASLSYILKAKNAGMSLGAKGAGLPSEAVOMLCHQAFIL 1080
1021 FHQVWKNPTFFLRISDTASLSYILKAKNAGMSLGAKGAGLPSEAVOMLCHQAFIL 1080
1081 KLTRHRTVYVPLGSLRTAQTOISRLKPLGTTTLTALEAANPALPSDFEFTIID 1132
1081 KLTRHRTVYVPLGSLRTAQTOISRLKPLGTTTLTALEAANPALPSDFEFTIID 1132
RESULT 20
US-10-044-539-2
Sequence 2, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
Applicant: Cech, Thomas R.
Inventor: Jochim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-044-539-2

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCARVRSILSHYREVLPATFVRLGPQGRRLVQSGDPAAPALVAQCIVCPM 60
DB 1 MPAPRCARVRSILSHYREVLPATFVRLGPQGRRLVQSGDPAAPALVAQCIVCPM 60

QY 61 DARPPAPASFRQVSCLELVARVLOQLCERGAKNVLAFFGALLDAGRGPEAFTTSVR 120
DB 61 DARPPAPASFRQVSCLELVARVLOQLCERGAKNVLAFFGALLDAGRGPEAFTTSVR 120

QY 121 STLPNTVDTALRGSGAWGLLRVGDVYHLLACALFVVAAPSCAVQVCGPPIYQGA 180
DB 121 STLPNTVDTALRGSGAWGLLRVGDVYHLLACALFVVAAPSCAVQVCGPPIYQGA 180

QY 181 ATQAPPPASGPRRLGGERAMNSVREAGVPLGLPAPGARRGSGASRLPLPKERR 240
DB 181 ATQAPPPASGPRRLGGERAMNSVREAGVPLGLPAPGARRGSGASRLPLPKERR 240

QY 241 GAAPERRPPVQGSVAHPGRTGSDRGFCVVASPARPEEXTSLEGLSGRHSHPVSG 300
DB 241 GAAPERRPPVQGSVAHPGRTGSDRGFCVVASPARPEEXTSLEGLSGRHSHPVSG 300

QY 301 RQHHAGPPTSPRPWDTPCPVYAETGFLYSSGDEKQLRPSFLSLSPSLTGARL 360
DB 301 RQHHAGPPTSPRPWDTPCPVYAETGFLYSSGDEKQLRPSFLSLSPSLTGARL 360

QY 361 VETIFGSRPMWPGTRRLPLPQRYWQMRPLFLELGNHACPGYVILKTHCPILAAVT 420

DB 361 VETIFGSRPMWPGTRRLPLPQRYWQMRPLFLELGNHACPGYVILKTHCPILAAVT 420

QY 421 PAAGVCAKPKQGSVAAPPEEDTPRRLVOLLROSSSPQVYGFVACLRRLVPGKMS 480
DB 421 PAAGVCAKPKQGSVAAPPEEDTPRRLVOLLROSSSPQVYGFVACLRRLVPGKMS 480

QY 481 RHNERFRLNTKFKISLGAKLSLOELTWKMSVDCALRRSPGVGCPAAEHRLREBI 540
DB 481 RHNERFRLNTKFKISLGAKLSLOELTWKMSVDCALRRSPGVGCPAAEHRLREBI 540

QY 541 LAFELHMSVYVELLRSPFYVTEFTFQNRLLFPFRBSVSKLQSIGRQLKRYQLE 600
DB 541 LAFELHMSVYVELLRSPFYVTEFTFQNRLLFPFRBSVSKLQSIGRQLKRYQLE 600

QY 601 LSEAEVROHEARPAULTSRPLFPKPDGRPIVMNDVYVGAARTPREGRARLTSRYA 660
DB 601 LSEAEVROHEARPAULTSRPLFPKPDGRPIVMNDVYVGAARTPREGRARLTSRYA 660

QY 661 LPSVLNERARBPGLIGASVLTGLDIDHRAKRTFVLRQAODPPPELYFVKVDVTGAYDTI 720
DB 661 LPSVLNERARBPGLIGASVLTGLDIDHRAKRTFVLRQAODPPPELYFVKVDVTGAYDTI 720

QY 721 PQRLTEVLASITKPNQTCVRRYAVQRAHGHAKAKSHVSTLTDQPTMRQPVHL 780
DB 721 PQRLTEVLASITKPNQTCVRRYAVQRAHGHAKAKSHVSTLTDQPTMRQPVHL 780

QY 781 QETSPLRDAVTLBOSSSLNEASSGLPDLRFMCHNAVIRKSYVQCGIPIQSGISTL 840
DB 781 QETSPLRDAVTLBOSSSLNEASSGLPDLRFMCHNAVIRKSYVQCGIPIQSGISTL 840

QY 841 LGLCLGDMENKLPAGIRBDGLLRVYDPLVTLPHLTHAKFLRLVNGVEYGVNVL 900
DB 841 LGLCLGDMENKLPAGIRBDGLLRVYDPLVTLPHLTHAKFLRLVNGVEYGVNVL 900

QY 901 RKTIVNFPVDEALGTAFAVQMPAHGLFPMCGILLDTFRLLEVQSDYSYARTSIRASVTF 960
DB 901 RKTIVNFPVDEALGTAFAVQMPAHGLFPMCGILLDTFRLLEVQSDYSYARTSIRASVTF 960

QY 961 NRGFKAQRNRKLPGLVLRKCHSLFLDQVNSLQVCTNIYKILLQVYRHACTQLP 1020
DB 961 NRGFKAQRNRKLPGLVLRKCHSLFLDQVNSLQVCTNIYKILLQVYRHACTQLP 1020

QY 1021 FHOQWKNPFFFLRVISDTASLCYSTLKXKNGMSLGAKGAAPLSEAVQWLCHQAFLL 1080
DB 1021 FHOQWKNPFFFLRVISDTASLCYSTLKXKNGMSLGAKGAAPLSEAVQWLCHQAFLL 1080

QY 1081 KLTRHRVTVPLGLSLRTAQQLSRKLPGTTTLTALEAANPALPSDFKTIID 1132
DB 1081 KLTRHRVTVPLGLSLRTAQQLSRKLPGTTTLTALEAANPALPSDFKTIID 1132

RESULT 21
US-10-295-681-57
Sequence 57, Application US/10295681
Publication No. US20030166270A1
GENERAL INFORMATION:
APPLICANT: E. Premkumar Reddy
APPLICANT: Sushil G. Rane
APPLICANT: Richard V. Metcus
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REVERSIBLY
INDUCING CONTINUAL GROWTH IN NORMAL CELLS
FILE REFERENCE: 6056-307
CURRENT APPLICATION NUMBER: US/10/295,681
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/334,760
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 57
LENGTH: 1132
TYPE: PRT
ORGANISM: Homo sapiens

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us-08-974-584c-118.rapb

Page 21

US-10-295-681-57

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRLSRSHREVLPLATFVRRLGPOGMRLVORGPAPFPAALVACLVCM 60
DB 1 MPAPRCRAVRLSRSHREVLPLATFVRRLGPOGMRLVORGPAPFPAALVACLVCM 60
QY 61 DAPPPAPSPROVSCIKELVAVLQRLCERGANVLAFLGALLDAGRGPPAFTTSVR 120
DB 61 DAPPPAPSPROVSCIKELVAVLQRLCERGANVLAFLGALLDAGRGPPAFTTSVR 120
QY 121 SYLPTVTDLRSGAMGLLRVGGDVVHLARQALPLVAPSCAYQCGPPLTQLA 180
DB 121 SYLPTVTDLRSGAMGLLRVGGDVVHLARQALPLVAPSCAYQCGPPLTQLA 180
QY 181 ATGARPPHAGSPRRRLGGERAMNHSYREAGVPLGJAPGARRRGSASRSLPLPRPRR 240
DB 181 ATGARPPHAGSPRRRLGGERAMNHSYREAGVPLGJAPGARRRGSASRSLPLPRPRR 240
QY 241 GAPEPERTVGGGSMHPRTRGSPDRGFCVSPAPAPAEATSLGALSGTRHSPSVG 300
DB 241 GAPEPERTVGGGSMHPRTRGSPDRGFCVSPAPAPAEATSLGALSGTRHSPSVG 300
QY 301 ROHAGPSTSRPPRPMDTCPPEVYATKHFLLYSSGDKQLRPSFLSLRPSLTGARL 360
DB 301 ROHAGPSTSRPPRPMDTCPPEVYATKHFLLYSSGDKQLRPSFLSLRPSLTGARL 360
QY 361 VETIFLGSRRPMDTCPPEVYATKHFLLYSSGDKQLRPSFLSLRPSLTGARL 420
DB 361 VETIFLGSRRPMDTCPPEVYATKHFLLYSSGDKQLRPSFLSLRPSLTGARL 420
QY 421 PAAGVCAKREKQSVAAPEEDTDPRLVQRLRQSSPMQVGFVRAACRLVPPSLMS 480
DB 421 PAAGVCAKREKQSVAAPEEDTDPRLVQRLRQSSPMQVGFVRAACRLVPPSLMS 480
QY 481 RHNERPFLRNTKKEFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCPAAEHLREBI 540
DB 481 RHNERPFLRNTKKEFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCPAAEHLREBI 540
QY 541 LAPELHMSVYVVELLRSEFFVTEFTFOQNRLEFFRPSWSTLQSIGRQHLKQVLE 600
DB 541 LAPELHMSVYVVELLRSEFFVTEFTFOQNRLEFFRPSWSTLQSIGRQHLKQVLE 600
QY 601 LSEAEVROHREARFALLTSRLRPIPKDGLRPIVNMDDVVGARTFRERKAEELTSRVA 660
DB 601 LSEAEVROHREARFALLTSRLRPIPKDGLRPIVNMDDVVGARTFRERKAEELTSRVA 660
QY 661 LSEVLYERARRRGLIGASVLSJDIHRAMRTFVLNRAODPPPELYFYKVDYTGAYDTI 720
DB 661 LSEVLYERARRRGLIGASVLSJDIHRAMRTFVLNRAODPPPELYFYKVDYTGAYDTI 720
QY 721 POURLTEVLASIKPONTYCVRRYAVVOKAHGVKAKAFKSHVSTLTDOPYMRQVAVL 780
DB 721 POURLTEVLASIKPONTYCVRRYAVVOKAHGVKAKAFKSHVSTLTDOPYMRQVAVL 780
QY 781 QETSPRLDAVAVIOSSSLNEASSGLFDVFLRFGCHHAVIRGKSYVQCGIPIQSGISLTL 840
DB 781 QETSPRLDAVAVIOSSSLNEASSGLFDVFLRFGCHHAVIRGKSYVQCGIPIQSGISLTL 840
QY 841 LQSLCYGDMENKLFAGIRBDGILLRLVDFELVTPHLTAKTFLRLVGVPEYGVAVL 900
DB 841 LQSLCYGDMENKLFAGIRBDGILLRLVDFELVTPHLTAKTFLRLVGVPEYGVAVL 900
QY 901 RKTIVNFPVEDEALGTAFAVQMAHGLFPWCGILLDTRILEVQSDVSARISIRASVTF 960
DB 901 RKTIVNFPVEDEALGTAFAVQMAHGLFPWCGILLDTRILEVQSDVSARISIRASVTF 960
QY 961 NRGFKAQRNRKRLFGVLRKCHSLPLDQVNSLQVCTNIXKILLQAVRHACVQLP 1020
DB 961 NRGFKAQRNRKRLFGVLRKCHSLPLDQVNSLQVCTNIXKILLQAVRHACVQLP 1020

QY 1021 FHQVWKMPTEPLRLISTASLCYSILKAKNAGSLGAKGAGPLPSAVOMLCHQAFLL 1080
DB 1021 FHQVWKMPTEPLRLISTASLCYSILKAKNAGSLGAKGAGPLPSAVOMLCHQAFLL 1080
QY 1081 KLRHRTVYVPLGSLRTAQOTLSRKLPGTTLTLEMAANPALPSDFKTIID 1132
DB 1081 KLRHRTVYVPLGSLRTAQOTLSRKLPGTTLTLEMAANPALPSDFKTIID 1132

RESULT 22
US-10-325-810-2
Sequence 2, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Czech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aussenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-325-810-2

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPRCRAVRSLSHRYEVLPLATFVRRLGPOGMRVLVORGDPAFRALVAQCLVCVFW 60
1 MRAPRCRAVRSLSHRYEVLPLATFVRRLGPOGMRVLVORGDPAFRALVAQCLVCVFW 60
DB 1 MRAPRCRAVRSLSHRYEVLPLATFVRRLGPOGMRVLVORGDPAFRALVAQCLVCVFW 60
QY 61 DARPPPAABSFQVSCLELVAVRVLQRLCERGAKNVLAFFGALLDGAAGPPEAFTTSVR 120
61 DARPPPAABSFQVSCLELVAVRVLQRLCERGAKNVLAFFGALLDGAAGPPEAFTTSVR 120
DB 61 DARPPPAABSFQVSCLELVAVRVLQRLCERGAKNVLAFFGALLDGAAGPPEAFTTSVR 120
QY 121 SYLPTNTVDALRSGAGWGLLRVGDVLYHLARCALFVLVAPSCAYGVCPPLYQIGA 180
121 SYLPTNTVDALRSGAGWGLLRVGDVLYHLARCALFVLVAPSCAYGVCPPLYQIGA 180
DB 121 SYLPTNTVDALRSGAGWGLLRVGDVLYHLARCALFVLVAPSCAYGVCPPLYQIGA 180
QY 181 ATQARPPPHASGRRRLGGERAMNHSVRBAGVPLGAPGARRRGGSASRSLLPKEPRR 240
181 ATQARPPPHASGRRRLGGERAMNHSVRBAGVPLGAPGARRRGGSASRSLLPKEPRR 240
DB 181 ATQARPPPHASGRRRLGGERAMNHSVRBAGVPLGAPGARRRGGSASRSLLPKEPRR 240
QY 241 GAAPBERPTVQGGSAHAPGRTGSDGFCVVSAPARAEATSLGALSGTRHSHPSVG 300
241 GAAPBERPTVQGGSAHAPGRTGSDGFCVVSAPARAEATSLGALSGTRHSHPSVG 300
DB 241 GAAPBERPTVQGGSAHAPGRTGSDGFCVVSAPARAEATSLGALSGTRHSHPSVG 300
QY 301 ROHHAGPSTSRPPRPMWDTCPVVAETKHFLYSSGDEQLRPSLLSLRPSLTGARTL 360
301 ROHHAGPSTSRPPRPMWDTCPVVAETKHFLYSSGDEQLRPSLLSLRPSLTGARTL 360
DB 301 ROHHAGPSTSRPPRPMWDTCPVVAETKHFLYSSGDEQLRPSLLSLRPSLTGARTL 360
QY 361 VETIFLGSRRPMMGTPRRRLPRLPQRYWQMRPLFLELLGNHACQPYGVILKTHCPRAAVT 420
361 VETIFLGSRRPMMGTPRRRLPRLPQRYWQMRPLFLELLGNHACQPYGVILKTHCPRAAVT 420
DB 361 VETIFLGSRRPMMGTPRRRLPRLPQRYWQMRPLFLELLGNHACQPYGVILKTHCPRAAVT 420
QY 421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLLRQHSSPMQVYGFVACLRRLVPPGLMGS 480
421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLLRQHSSPMQVYGFVACLRRLVPPGLMGS 480
DB 421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLLRQHSSPMQVYGFVACLRRLVPPGLMGS 480
QY 481 RHNERRFLNNTKFTSLGHAHLSTQELTWKMSVDCAMLRSPGVCGVPAEHRRLREI 540
481 RHNERRFLNNTKFTSLGHAHLSTQELTWKMSVDCAMLRSPGVCGVPAEHRRLREI 540
DB 481 RHNERRFLNNTKFTSLGHAHLSTQELTWKMSVDCAMLRSPGVCGVPAEHRRLREI 540
QY 541 LAKFLHMLMSVYVVELLRSEFFVETTTQKNLFYRPSVMSKLOSLGRHLKRVQRE 600
541 LAKFLHMLMSVYVVELLRSEFFVETTTQKNLFYRPSVMSKLOSLGRHLKRVQRE 600
DB 541 LAKFLHMLMSVYVVELLRSEFFVETTTQKNLFYRPSVMSKLOSLGRHLKRVQRE 600
QY 601 LSEAEVRQHRERAPALITSLRFLPKPDGLRPIVMMDYVGARTERREKAERLTSRYKA 660
601 LSEAEVRQHRERAPALITSLRFLPKPDGLRPIVMMDYVGARTERREKAERLTSRYKA 660
DB 601 LSEAEVRQHRERAPALITSLRFLPKPDGLRPIVMMDYVGARTERREKAERLTSRYKA 660
QY 661 LRSVLYNERARRPGLIGASVGLDIDIRAMRTFVRYAODPPPELYVWVDVYGAFTT 720
661 LRSVLYNERARRPGLIGASVGLDIDIRAMRTFVRYAODPPPELYVWVDVYGAFTT 720
DB 661 LRSVLYNERARRPGLIGASVGLDIDIRAMRTFVRYAODPPPELYVWVDVYGAFTT 720
QY 721 PODRLTEVIASTIKPONTVCARVAVVOGAHGHYRKAFKSHVSTLTLDQPYMRQFVHL 780
721 PODRLTEVIASTIKPONTVCARVAVVOGAHGHYRKAFKSHVSTLTLDQPYMRQFVHL 780
DB 721 PODRLTEVIASTIKPONTVCARVAVVOGAHGHYRKAFKSHVSTLTLDQPYMRQFVHL 780
QY 781 QETSPILRDAVITBOSSSLNEASSGLFDVFLRPMCHAVIRKSKSYVQCGIPQGSILSTL 840
781 QETSPILRDAVITBOSSSLNEASSGLFDVFLRPMCHAVIRKSKSYVQCGIPQGSILSTL 840
DB 781 QETSPILRDAVITBOSSSLNEASSGLFDVFLRPMCHAVIRKSKSYVQCGIPQGSILSTL 840
QY 841 LGSICVGDMENTLFGIRRDGLLRVDPFLVTPHLTHAKTFLTLVARGVPEYCVNVL 900
841 LGSICVGDMENTLFGIRRDGLLRVDPFLVTPHLTHAKTFLTLVARGVPEYCVNVL 900
DB 841 LGSICVGDMENTLFGIRRDGLLRVDPFLVTPHLTHAKTFLTLVARGVPEYCVNVL 900
QY 901 RKTVVNFPEEDALGGTAFCVQPAHGLFPWCGLLIDTRTLEVOSSDYSSVARTSIRASVTF 960
901 RKTVVNFPEEDALGGTAFCVQPAHGLFPWCGLLIDTRTLEVOSSDYSSVARTSIRASVTF 960
DB 901 RKTVVNFPEEDALGGTAFCVQPAHGLFPWCGLLIDTRTLEVOSSDYSSVARTSIRASVTF 960
QY 961 NRGFKAGRMRRKLFQVLAELKCHSLFLDQVNSLQTVCTNIXIILLQAYRFAHCVQLDP 1020
961 NRGFKAGRMRRKLFQVLAELKCHSLFLDQVNSLQTVCTNIXIILLQAYRFAHCVQLDP 1020
DB 961 NRGFKAGRMRRKLFQVLAELKCHSLFLDQVNSLQTVCTNIXIILLQAYRFAHCVQLDP 1020

RESULT 23
US-10-388-578-2
Sequence 2, Application US/10388578
Publication No. US20030224411A1
GENERAL INFORMATION:
APPLICANT: Geron Corporation
APPLICANT: Stanton, Lawrence
APPLICANT: Ralph, Brandeberger
APPLICANT: Joseph, Gold D.
APPLICANT: John, Irving
APPLICANT: Mandalam, Ramkumar
APPLICANT: Mok, Michael
APPLICANT: Shelton, Dawne
TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of Human Embryonic Stem Cells
FILE REFERENCE: 135/001
CURRENT APPLICATION NUMBER: US/10/388,578
CURRENT FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 139
SOFTWARE: Custom
SEQ ID NO 2
LENGTH: 1132
TYPE: PRT
ORGANISM: Homo sapiens
US-10-388-578-2

Query Match 99.8%; Score 5952; DB 14; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPRCRAVRSLSHRYEVLPLATFVRRLGPOGMRVLVORGDPAFRALVAQCLVCVFW 60
1 MRAPRCRAVRSLSHRYEVLPLATFVRRLGPOGMRVLVORGDPAFRALVAQCLVCVFW 60
DB 1 MRAPRCRAVRSLSHRYEVLPLATFVRRLGPOGMRVLVORGDPAFRALVAQCLVCVFW 60
QY 61 DARPPPAABSFQVSCLELVAVRVLQRLCERGAKNVLAFFGALLDGAAGPPEAFTTSVR 120
61 DARPPPAABSFQVSCLELVAVRVLQRLCERGAKNVLAFFGALLDGAAGPPEAFTTSVR 120
DB 61 DARPPPAABSFQVSCLELVAVRVLQRLCERGAKNVLAFFGALLDGAAGPPEAFTTSVR 120
QY 121 SYLPTNTVDALRSGAGWGLLRVGDVLYHLARCALFVLVAPSCAYGVCPPLYQIGA 180
121 SYLPTNTVDALRSGAGWGLLRVGDVLYHLARCALFVLVAPSCAYGVCPPLYQIGA 180
DB 121 SYLPTNTVDALRSGAGWGLLRVGDVLYHLARCALFVLVAPSCAYGVCPPLYQIGA 180
QY 181 ATQARPPPHASGRRRLGGERAMNHSVRBAGVPLGAPGARRRGGSASRSLLPKEPRR 240
181 ATQARPPPHASGRRRLGGERAMNHSVRBAGVPLGAPGARRRGGSASRSLLPKEPRR 240
DB 181 ATQARPPPHASGRRRLGGERAMNHSVRBAGVPLGAPGARRRGGSASRSLLPKEPRR 240
QY 241 GAAPBERPTVQGGSAHAPGRTGSDGFCVVSAPARAEATSLGALSGTRHSHPSVG 300
241 GAAPBERPTVQGGSAHAPGRTGSDGFCVVSAPARAEATSLGALSGTRHSHPSVG 300
DB 241 GAAPBERPTVQGGSAHAPGRTGSDGFCVVSAPARAEATSLGALSGTRHSHPSVG 300
QY 301 ROHHAGPSTSRPPRPMWDTCPVVAETKHFLYSSGDEQLRPSLLSLRPSLTGARTL 360
301 ROHHAGPSTSRPPRPMWDTCPVVAETKHFLYSSGDEQLRPSLLSLRPSLTGARTL 360
DB 301 ROHHAGPSTSRPPRPMWDTCPVVAETKHFLYSSGDEQLRPSLLSLRPSLTGARTL 360
QY 361 VETIFLGSRRPMMGTPRRRLPRLPQRYWQMRPLFLELLGNHACQPYGVILKTHCPRAAVT 420
361 VETIFLGSRRPMMGTPRRRLPRLPQRYWQMRPLFLELLGNHACQPYGVILKTHCPRAAVT 420
DB 361 VETIFLGSRRPMMGTPRRRLPRLPQRYWQMRPLFLELLGNHACQPYGVILKTHCPRAAVT 420
QY 421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLLRQHSSPMQVYGFVACLRRLVPPGLMGS 480
421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLLRQHSSPMQVYGFVACLRRLVPPGLMGS 480
DB 421 PAAGVAREKPGQSVAAPEEDTDPRRLVQLLRQHSSPMQVYGFVACLRRLVPPGLMGS 480

QY 481 RHNERRLRNTKFKFISLQKNAKLSLOELTWKMSVRDCAMLRSPGVGCVPAEHRRLREI 540
 DB 481 RHNERRLRNTKFKFISLQKNAKLSLOELTWKMSVRDCAMLRSPGVGCVPAEHRRLREI 540
 QY 541 LAKFLHMLMSYVVELLSRFYVETTFQKXRLFFRYPSWMSKQSIGIRHKLKVQJRE 600
 DB 541 LAKFLHMLMSYVVELLSRFYVETTFQKXRLFFRYPSWMSKQSIGIRHKLKVQJRE 600
 QY 601 LSEAEVRQHRERARPPALTLSTRLEFIPKPDGLPIVMDVYVGARTFRREKAEELTSVKA 660
 DB 601 LSEAEVRQHRERARPPALTLSTRLEFIPKPDGLPIVMDVYVGARTFRREKAEELTSVKA 660
 QY 661 LFSVLYNERARPPALTLSTRLEFIPKPDGLPIVMDVYVGARTFRREKAEELTSVKA 660
 DB 661 LFSVLYNERARPPALTLSTRLEFIPKPDGLPIVMDVYVGARTFRREKAEELTSVKA 660
 QY 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAHGVRAKFKSHVSTLTDLPYMRQFVAHL 780
 DB 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAHGVRAKFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPFLDAVYIEGSSSLNEASGSLFDVFLRPMCHAVRIRGKSYVQCGIPQGSILSTL 840
 DB 781 QETSPFLDAVYIEGSSSLNEASGSLFDVFLRPMCHAVRIRGKSYVQCGIPQGSILSTL 840
 QY 841 LCSLCYGDMMENKLPAGIRRDGILLRLVDDFLVTHLTHAKTFLRTLVRGVEYGCYNL 900
 DB 841 LCSLCYGDMMENKLPAGIRRDGILLRLVDDFLVTHLTHAKTFLRTLVRGVEYGCYNL 900
 QY 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGLLDRLTEVQSDYSYARTSIRASVTE 960
 DB 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGLLDRLTEVQSDYSYARTSIRASVTE 960
 QY 961 NRGFAGNNMRKLPGLVRLKCHSLFLDLQVNSIQYVCTNIYKILLQAVRFACVQLP 1020
 DB 961 NRGFAGNNMRKLPGLVRLKCHSLFLDLQVNSIQYVCTNIYKILLQAVRFACVQLP 1020
 QY 1021 FHQGVWKNPTEFLFVISTDLSLCSILKAKNAGMSLGAAGAFLPSEAVQMLCHQAFIL 1080
 DB 1021 FHQGVWKNPTEFLFVISTDLSLCSILKAKNAGMSLGAAGAFLPSEAVQMLCHQAFIL 1080
 QY 1081 KTRHRVTVVPLIGSLRTAQTOLSRKLPGLTTLTALEAANPALPSDFKTLID 1132
 DB 1081 KTRHRVTVVPLIGSLRTAQTOLSRKLPGLTTLTALEAANPALPSDFKTLID 1132

RESULT 24
 US-10-602-441-2
 ; Sequence 2, Application US/10602441
 ; Publication No. US20040106128A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Geron Corporation
 ; APPLICANT: Majumdar, Anish Sen
 ; APPLICANT: Ferber, Iris
 ; APPLICANT: Frolkis, Maria
 ; APPLICANT: Wang, Zhuo
 ; TITLE OF INVENTION: Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase Reve
 ; FILE REFERENCE: 086/002
 ; CURRENT APPLICATION NUMBER: US/10/602,441
 ; PRIOR FILING DATE: 2003-06-24
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 1132
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 US-10-602-441-2

Query Match 99.8%; Score 5952; DB 16; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPRAPCRAVRSLASHYREVLPATFVRRLGPOGMRLVORDDPAFPAFVAVQCLVCPW 60
 DB 1 MPRAPCRAVRSLASHYREVLPATFVRRLGPOGMRLVORDDPAFPAFVAVQCLVCPW 60
 QY 61 DARPPPAASFRQVSLKELVAVVQLRCEKAKNVLAFGPALLDGAAGGPEAFTTSVR 120
 DB 61 DARPPPAASFRQVSLKELVAVVQLRCEKAKNVLAFGPALLDGAAGGPEAFTTSVR 120
 QY 121 SYLPTVTDALRGSGAMGILLRVGDDVTHLAAICALFVYVAPSCAYOVGPRYQJGA 180
 DB 121 SYLPTVTDALRGSGAMGILLRVGDDVTHLAAICALFVYVAPSCAYOVGPRYQJGA 180
 QY 181 ATQARPPPHASGPRRLCGERAMNHSVEAGVPLGLPAPGARRRGSGASRSLPLPKRPR 240
 DB 181 ATQARPPPHASGPRRLCGERAMNHSVEAGVPLGLPAPGARRRGSGASRSLPLPKRPR 240
 QY 241 GAAPPERTPVQGSMAHPRGTRGSDRGFCVSPAPAPAEATSLFGLSGTRHSHPSVG 300
 DB 241 GAAPPERTPVQGSMAHPRGTRGSDRGFCVSPAPAPAEATSLFGLSGTRHSHPSVG 300
 QY 301 ROHHAQPPSTSRPPAMDTPCPVYAEKTHFLYSSGDKEQLRPSFLSLRPSLIGARL 360
 DB 301 ROHHAQPPSTSRPPAMDTPCPVYAEKTHFLYSSGDKEQLRPSFLSLRPSLIGARL 360
 QY 361 VETIFLSRPMWGPTRPLPRLPQRYWQMRPLFELLGNHAQCPYGVLLKTHCPRLAAVT 420
 DB 361 VETIFLSRPMWGPTRPLPRLPQRYWQMRPLFELLGNHAQCPYGVLLKTHCPRLAAVT 420
 QY 421 PAAGVCAEKKQGSAAAEEDTDBRLVOLLROHSSWQYGFACRLRLVPPGLMS 480
 DB 421 PAAGVCAEKKQGSAAAEEDTDBRLVOLLROHSSWQYGFACRLRLVPPGLMS 480
 QY 481 RHNERRLRNTKFKFISLQKNAKLSLOELTWKMSVRDCAMLRSPGVGCVPAEHRRLREI 540
 DB 481 RHNERRLRNTKFKFISLQKNAKLSLOELTWKMSVRDCAMLRSPGVGCVPAEHRRLREI 540
 QY 541 LAKFLHMLMSYVVELLSRFYVETTFQKXRLFFRYPSWMSKQSIGIRHKLKVQJRE 600
 DB 541 LAKFLHMLMSYVVELLSRFYVETTFQKXRLFFRYPSWMSKQSIGIRHKLKVQJRE 600
 QY 601 LSEAEVRQHRERARPPALTLSTRLEFIPKPDGLPIVMDVYVGARTFRREKAEELTSVKA 660
 DB 601 LSEAEVRQHRERARPPALTLSTRLEFIPKPDGLPIVMDVYVGARTFRREKAEELTSVKA 660
 QY 661 LFSVLYNERARPPALTLSTRLEFIPKPDGLPIVMDVYVGARTFRREKAEELTSVKA 660
 DB 661 LFSVLYNERARPPALTLSTRLEFIPKPDGLPIVMDVYVGARTFRREKAEELTSVKA 660
 QY 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAHGVRAKFKSHVSTLTDLPYMRQFVAHL 780
 DB 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAHGVRAKFKSHVSTLTDLPYMRQFVAHL 780
 QY 781 QETSPFLDAVYIEGSSSLNEASGSLFDVFLRPMCHAVRIRGKSYVQCGIPQGSILSTL 840
 DB 781 QETSPFLDAVYIEGSSSLNEASGSLFDVFLRPMCHAVRIRGKSYVQCGIPQGSILSTL 840
 QY 841 LCSLCYGDMMENKLPAGIRRDGILLRLVDDFLVTHLTHAKTFLRTLVRGVEYGCYNL 900
 DB 841 LCSLCYGDMMENKLPAGIRRDGILLRLVDDFLVTHLTHAKTFLRTLVRGVEYGCYNL 900
 QY 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGLLDRLTEVQSDYSYARTSIRASVTE 960
 DB 901 RKTIVNPFVEDEALGTAFAVQMPAHGLFPMCGLLDRLTEVQSDYSYARTSIRASVTE 960
 QY 961 NRGFAGNNMRKLPGLVRLKCHSLFLDLQVNSIQYVCTNIYKILLQAVRFACVQLP 1020
 DB 961 NRGFAGNNMRKLPGLVRLKCHSLFLDLQVNSIQYVCTNIYKILLQAVRFACVQLP 1020
 QY 1021 FHQGVWKNPTEFLFVISTDLSLCSILKAKNAGMSLGAAGAFLPSEAVQMLCHQAFIL 1080
 DB 1021 FHQGVWKNPTEFLFVISTDLSLCSILKAKNAGMSLGAAGAFLPSEAVQMLCHQAFIL 1080

QY 1081 KLTRHRVTYVPLGSLRTAQTOLSRKLPQTTLTALAAANPALPSDFKTIID 1132
 DB 1081 KLTRHRVTYVPLGSLRTAQTOLSRKLPQTTLTALAAANPALPSDFKTIID 1132

RESULT 25

US-10-389-431-2
 ; Sequence 2, Application US/10389431
 ; Publication No. US20040180347A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genon Corporation
 ; APPLICANT: Stanton, Lawrence
 ; APPLICANT: Ralph, Brandenberger
 ; APPLICANT: Joseph, Gold D.
 ; APPLICANT: John, Irving
 ; APPLICANT: Mandalam, Ramkumar
 ; APPLICANT: Mok, Michael
 ; TITLE OF INVENTION: A Marker System for Preparing and Characterizing High-Quality Hum
 ; FILE REFERENCE: 135/002
 ; CURRENT APPLICATION NUMBER: US/10/389,431
 ; CURRENT FILING DATE: 2003-03-13
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 1132
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-389-431-2

Query Match 99.8%; Score 5952; DB 16; Length 1132;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRRAPRCRAVRSLSLRSHYREVLPLATFVRRLGPGQMRVLVQRGDPAPAFALVAQCIVCPM 60
 DB 1 MRRAPRCRAVRSLSLRSHYREVLPLATFVRRLGPGQMRVLVQRGDPAPAFALVAQCIVCPM 60
 QY 61 DARPPPAASFRQVSTLKEVLVARVLOQLCEBGAQVLAFFGLLGGAGGPEARTTSVR 120
 DB 61 DARPPPAASFRQVSTLKEVLVARVLOQLCEBGAQVLAFFGLLGGAGGPEARTTSVR 120
 QY 121 SYLENTVTALRSGAGMGLLRRVGDVVLHLLARCAFLVLAAPSACAYQVCPPLYLQGA 180
 DB 121 SYLENTVTALRSGAGMGLLRRVGDVVLHLLARCAFLVLAAPSACAYQVCPPLYLQGA 180
 QY 181 ATQARPPPHASGRRRLGCEPAMNHSVREAGVPLGIPAGARRRGSASRSLLPKRRR 240
 DB 181 ATQARPPPHASGRRRLGCEPAMNHSVREAGVPLGIPAGARRRGSASRSLLPKRRR 240
 QY 241 GAAPBERTPVGGGSAHAGRTRGSPDRGFCVSPARPAEBATSLGALSGTRHSHPSVG 300
 DB 241 GAAPBERTPVGGGSAHAGRTRGSPDRGFCVSPARPAEBATSLGALSGTRHSHPSVG 300
 QY 301 RQHHAGPSTSRPBPMDTPCPVVAETKGFLLYSSGDKQLRPSTLLSLRPSLTGARRL 360
 DB 301 RQHHAGPSTSRPBPMDTPCPVVAETKGFLLYSSGDKQLRPSTLLSLRPSLTGARRL 360
 QY 361 VETIFLGSRRPWPMPGTGRRRLPRLPORWQMRPLFELIGNHACCPYGLTKTCPLRAVLT 420
 DB 361 VETIFLGSRRPWPMPGTGRRRLPRLPORWQMRPLFELIGNHACCPYGLTKTCPLRAVLT 420
 QY 421 PAAGVACAREKPOGSAVAPEEDTDPRLVQLLRHSSPWQVGYFARACLRRLVPPGLMGS 480
 DB 421 PAAGVACAREKPOGSAVAPEEDTDPRLVQLLRHSSPWQVGYFARACLRRLVPPGLMGS 480
 QY 481 RHHERFPLNTKKFISLGHAKLSLOELTWKSVNDCAWLRSPOGVCVPAEHLREI 540
 DB 481 RHHERFPLNTKKFISLGHAKLSLOELTWKSVNDCAWLRSPOGVCVPAEHLREI 540
 QY 541 LAKFLHMLSVYVVELLSFFVYTTETTFQKRLFFYRPSVSKLOSIGIRQLKXQVURE 600
 DB 541 LAKFLHMLSVYVVELLSFFVYTTETTFQKRLFFYRPSVSKLOSIGIRQLKXQVURE 600

DB 541 LAKFLHMLSVYVVELLSFFVYTTETTFQKRLFFYRPSVSKLOSIGIRQLKXQVURE 600
 QY 601 LSEAEVROHREANPALLTSRLREIFPKDGLRPIVMNDVYVAGATRRERKARLTSRYKA 660
 DB 601 LSEAEVROHREANPALLTSRLREIFPKDGLRPIVMNDVYVAGATRRERKARLTSRYKA 660
 QY 661 LFSVLNTERARRPGLIGASVLDGIDHRAHRTFVLNRAQDDPPELYFYKAVVTGAYDTI 720
 DB 661 LFSVLNTERARRPGLIGASVLDGIDHRAHRTFVLNRAQDDPPELYFYKAVVTGAYDTI 720
 QY 721 PQDRLTEVIASIKPONTYCVRRYAVYQAKAGHVRKAFKSHVSTLTDLOPYMRQFVAL 780
 DB 721 PQDRLTEVIASIKPONTYCVRRYAVYQAKAGHVRKAFKSHVSTLTDLOPYMRQFVAL 780
 QY 781 QETSPLRDVAVITQSSSLNEASGLDVLFRMCHHAHVRIRKSYVQCCGIGQSTLSLT 840
 DB 781 QETSPLRDVAVITQSSSLNEASGLDVLFRMCHHAHVRIRKSYVQCCGIGQSTLSLT 840
 QY 841 LGSICGDMENKLPAGIRRDGLLRVDPFLVTPHLTAKTFLTLVNGVEBGCVAL 900
 DB 841 LGSICGDMENKLPAGIRRDGLLRVDPFLVTPHLTAKTFLTLVNGVEBGCVAL 900
 QY 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVOQSDYSYAKTSIRASLTF 960
 DB 901 RKTIVNFPVEDEALGTAFAVQMPAHGLFPMCGLLDTRTLEVOQSDYSYAKTSIRASLTF 960
 QY 961 NRGFKAGNRMRKLPGLVRLKCHSLFLDQVNSLQTCVNTIKILLQAYRFAVCLQHP 1020
 DB 961 NRGFKAGNRMRKLPGLVRLKCHSLFLDQVNSLQTCVNTIKILLQAYRFAVCLQHP 1020
 QY 1021 FHQVWKNPFFFLRVISDTASLCYSILKAKNAGMSIGAKGAAGPLPSEAVQWLCHQAFLL 1080
 DB 1021 FHQVWKNPFFFLRVISDTASLCYSILKAKNAGMSIGAKGAAGPLPSEAVQWLCHQAFLL 1080
 QY 1081 KLTRHRVTYVPLGSLRTAQTOLSRKLPQTTLTALAAANPALPSDFKTIID 1132
 DB 1081 KLTRHRVTYVPLGSLRTAQTOLSRKLPQTTLTALAAANPALPSDFKTIID 1132

RESULT 26

US-10-877-124-2
 ; Sequence 2, Application US/10877124
 ; Publication No. US20040242529A1

GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingham, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Hartley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/877,124
 FILING DATE: 24-Jun-2004
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/432,503
 FILING DATE: 02-Nov-1999
 APPLICATION NUMBER: 08/974,549

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FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-877-124-2

Query Match      99.8%; Score 5952; DB 17; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAAPRCAGVSLRSHYREVLPLATFVRRLGPGGMRLVORGDPAPAFRALVACLVCPV 60
DB 1 MPRAAPRCAGVSLRSHYREVLPLATFVRRLGPGGMRLVORGDPAPAFRALVACLVCPV 60
QY 61 DAPPPAPASFRQVSCLEKELVAVYLQRLCERGANVLAFGFALIDGARGGPPPEAFTTSVR 120
DB 61 DAPPPAPASFRQVSCLEKELVAVYLQRLCERGANVLAFGFALIDGARGGPPPEAFTTSVR 120
QY 121 SYLNTVTDALRSGGANGMLLRVGDVLYVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRSGGANGMLLRVGDVLYVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATOARPPPHASGPRRLGCEERAMNHSVREAGVPLGLPAPGARRRGSSASSLPLPKPRR 240
DB 181 ATOARPPPHASGPRRLGCEERAMNHSVREAGVPLGLPAPGARRRGSSASSLPLPKPRR 240
QY 241 GAAPERTPTVYGQSMAPRGTRGSPDRGFCVSPAPPAEATSLSEALSGTRSHSVG 300
DB 241 GAAPERTPTVYGQSMAPRGTRGSPDRGFCVSPAPPAEATSLSEALSGTRSHSVG 300
QY 301 ROHAGPSTSRPRPMDTCCPPYVATKHFLLSSGDKQLRPSFLLSLRPSLTGARRL 360
DB 301 ROHAGPSTSRPRPMDTCCPPYVATKHFLLSSGDKQLRPSFLLSLRPSLTGARRL 360
QY 361 VETIFLGRPMWPGTPRRLPRLPORYWQMRPLFELLGNHAQCYGYLTKHCPRAVLT 420
DB 361 VETIFLGRPMWPGTPRRLPRLPORYWQMRPLFELLGNHAQCYGYLTKHCPRAVLT 420
QY 421 PAAGVCAEKPQGSAAPEEEDTPRRLVOLLROHSSPMQVYGFVRACTRLVPPGJMG 480
DB 421 PAAGVCAEKPQGSAAPEEEDTPRRLVOLLROHSSPMQVYGFVRACTRLVPPGJMG 480
QY 481 RHNERFLRNTKFTSLGKAHLSTQELTWKSVYDCAMLRSPGVGCVPAEHRLEETI 540
DB 481 RHNERFLRNTKFTSLGKAHLSTQELTWKSVYDCAMLRSPGVGCVPAEHRLEETI 540

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DB 481 RHNERFLRNTKFTSLGKAHLSTQELTWKSVYDCAMLRSPGVGCVPAEHRLEETI 540
QY 541 LAKFHMIMSYVYVVELLSFFVYETTTQKRLFFPRSVWSKOSTIQRHLKRVQURE 600
DB 541 LAKFHMIMSYVYVVELLSFFVYETTTQKRLFFPRSVWSKOSTIQRHLKRVQURE 600
QY 601 LSEAEVRQHREARPPALITSRLRFIPKPDGLRPIVMDVYVAGARTPREKEARELTSRYKA 660
DB 601 LSEAEVRQHREARPPALITSRLRFIPKPDGLRPIVMDVYVAGARTPREKEARELTSRYKA 660
QY 661 LFSVINYERARRPGLGASVYGLDDIHPAMTFVLVFAADPPPELIVKYVDVTCAYDTI 720
DB 661 LFSVINYERARRPGLGASVYGLDDIHPAMTFVLVFAADPPPELIVKYVDVTCAYDTI 720
QY 721 PDRLTEVIASITIKQNTYCVRYAVVOKAAGHVRKAFKSHVSTLTLOPYMRQFVAHL 780
DB 721 PDRLTEVIASITIKQNTYCVRYAVVOKAAGHVRKAFKSHVSTLTLOPYMRQFVAHL 780
QY 781 QETSPLRDAVVEIQSSINAEASGLFVFLRFMCHAVRIGKSYVCCGIPQGSILSTL 840
DB 781 QETSPLRDAVVEIQSSINAEASGLFVFLRFMCHAVRIGKSYVCCGIPQGSILSTL 840
QY 841 LCLCYGDMENKLFAGIRRDGLRLVDDPLVPLVTHAKTFLTLVAGVBEYGVNVL 900
DB 841 LCLCYGDMENKLFAGIRRDGLRLVDDPLVPLVTHAKTFLTLVAGVBEYGVNVL 900
QY 901 RKTIVNFPVEDALGTAFCVQMPAHGLFPWCGILDTRELEVQSDYSSYARTISASVTF 960
DB 901 RKTIVNFPVEDALGTAFCVQMPAHGLFPWCGILDTRELEVQSDYSSYARTISASVTF 960
QY 961 NRGFFAGNRMRKLFQVRLKCHSLFDLQVNSLCTVCTNLYKILLQARYFAVYQLP 1020
DB 961 NRGFFAGNRMRKLFQVRLKCHSLFDLQVNSLCTVCTNLYKILLQARYFAVYQLP 1020
QY 1021 FHOQVWKNTPFLRYSIDTASLCYSLKAKVAGSLGAKGAGPLPSAVQMLCHQATLL 1080
DB 1021 FHOQVWKNTPFLRYSIDTASLCYSLKAKVAGSLGAKGAGPLPSAVQMLCHQATLL 1080
QY 1081 KLTRRRTVYVPLGSLRTAQOTLSRKLPGTTLTLEAANPALPSDFXTIID 1132
DB 1081 KLTRRRTVYVPLGSLRTAQOTLSRKLPGTTLTLEAANPALPSDFXTIID 1132

RESULT 27
US-10-877-022-2
; Sequence 2, Application US/10877022
; Publication No. US20040247613A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
            Lingner, Joachim
            Nakamura, Toru
            Chapman, Karen B.
            Morin, Gregg B.
            Harley, Calvin B.
            Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,022
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-NOV-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-877-022-2

Query Match      99.8%; Score 5952; DB 17; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRAPRCRAVRSLSLRSHYREVLIATFVRRLRIGPOGRVLVORGDPAFAFLVAQCICVCPW 60
DB 1 MRAPRCRAVRSLSLRSHYREVLIATFVRRLRIGPOGRVLVORGDPAFAFLVAQCICVCPW 60
QY 61 DARPPPAASFRVOSCLKEIVARVLQRLCERGAKNVLAFGFALLDGARGPPEAFTTSVR 120
DB 61 DARPPPAASFRVOSCLKEIVARVLQRLCERGAKNVLAFGFALLDGARGPPEAFTTSVR 120
QY 121 SYLPNTVTALSGSGWGLLRVGDVIVHLLACALFVLYABSCAYQVCGPPLYQIGA 180
DB 121 SYLPNTVTALSGSGWGLLRVGDVIVHLLACALFVLYABSCAYQVCGPPLYQIGA 180
QY 181 ATQARPPPAASGPRRLRCERAMNHSVREAGVPLGLPAGARRRGSASRSLLPKRRR 240
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QY 241 GAAPBEERTPVCGSWAHPGRTGSDRGFCVVASPARPAEATSLGALSGTRHSHSVG 300
DB 241 GAAPBEERTPVCGSWAHPGRTGSDRGFCVVASPARPAEATSLGALSGTRHSHSVG 300
QY 301 RQHHAQPPSTSPRPWDTPCPVYAETGHLFYSGGKQOLRPSFLSLPSLTGARL 360
DB 301 RQHHAQPPSTSPRPWDTPCPVYAETGHLFYSGGKQOLRPSFLSLPSLTGARL 360
QY 361 VETIFLGSRRPMGTPRLRLPQRYWQRPFLLELGNHAQCPYVILLKTHCPRAAVT 420
DB 361 VETIFLGSRRPMGTPRLRLPQRYWQRPFLLELGNHAQCPYVILLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQSSPMQVYGFRACTLRLLVPGLMGS 480
DB 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQSSPMQVYGFRACTLRLLVPGLMGS 480

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DB 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQSSPMQVYGFRACTLRLLVPGLMGS 480
QY 481 RHNRRLRLNTKKFISLGKAKLSLOELTWKMSVRCAMLRBPQVCPVPAARLRREI 540
DB 481 RHNRRLRLNTKKFISLGKAKLSLOELTWKMSVRCAMLRBPQVCPVPAARLRREI 540
QY 541 LAKELHMLSVYVELLSFFVYETTFQKNRLFFRPSWSKLOSIGIRHILKRYOLBE 600
DB 541 LAKELHMLSVYVELLSFFVYETTFQKNRLFFRPSWSKLOSIGIRHILKRYOLBE 600
QY 601 LSEAEVTOHREARPAALITSLRLIPKPDGLRPVNMNDYVYGATTPREKRAEPLTRVYA 660
DB 601 LSEAEVTOHREARPAALITSLRLIPKPDGLRPVNMNDYVYGATTPREKRAEPLTRVYA 660
QY 661 LFSVLANERARRPGLIGASVIGDDIHRARTVLRADQPPPELIFYKVDVYAGYDTI 720
DB 661 LFSVLANERARRPGLIGASVIGDDIHRARTVLRADQPPPELIFYKVDVYAGYDTI 720
QY 721 PODRLTEVIASITIKPQNTYCVRRYAVQKAHGHVKAFFKSHVSTLTDIQPYWRQFVAHL 780
DB 721 PODRLTEVIASITIKPQNTYCVRRYAVQKAHGHVKAFFKSHVSTLTDIQPYWRQFVAHL 780
QY 781 QETSPLBDVAVIEOSSSLNEASSGLPDVPLRFPMCHAVIRGKSYVQCGIPQGSILSTL 840
DB 781 QETSPLBDVAVIEOSSSLNEASSGLPDVPLRFPMCHAVIRGKSYVQCGIPQGSILSTL 840
QY 841 LCSLCYGDMEKMLFAGIRBDGLLRVDDFLVTPHLTHAKFLRLVGRVEYGCVAL 900
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QY 901 RKTIVANFVDEALGGAFFQMPAHGLFPWCGLLDTRILEVQSDSSVARSISRLSTF 960
DB 901 RKTIVANFVDEALGGAFFQMPAHGLFPWCGLLDTRILEVQSDSSVARSISRLSTF 960
QY 961 NRQFKAGRNRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIVYLLIQAYRFAVCYOLP 1020
DB 961 NRQFKAGRNRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIVYLLIQAYRFAVCYOLP 1020
QY 1021 FHOQVMKNPFFFLRVISDTASLCYSILKAKNAGMSIGANGAOPLPSEAVOMLCHQAFLL 1080
DB 1021 FHOQVMKNPFFFLRVISDTASLCYSILKAKNAGMSIGANGAOPLPSEAVOMLCHQAFLL 1080
QY 1081 KLTRHRATVYPLGLSRLTAQTOLSRKLPGTTLTALPAANPALPSPFKIILD 1132
DB 1081 KLTRHRATVYPLGLSRLTAQTOLSRKLPGTTLTALPAANPALPSPFKIILD 1132

RESULT 28
US-10-044-692-323
Sequence 323, Application US/10044692
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Mortin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESS: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/044,692
  FILING DATE: 11-Jan-2002
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/912,951
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US 08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US 08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
  NAME: Apple, Randolph T.
  REGISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 323:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1154 amino acids
    TYPE: amino acid
    STRANDEDNESS: <Unknown>
    TOPOLOGY: linear
    MOLECULE TYPE: protein
    SEQUENCE DESCRIPTION: SEQ ID NO: 323:
US-10-044-692-323

Query Match      99.8%; Score 5952; DB 14; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCAVRSILRSYREYVLPATFVRRLPGQGMVLVORGPAPARALVACLVCPW 60
DB 1 MPRAPRCAVRSILRSYREYVLPATFVRRLPGQGMVLVORGPAPARALVACLVCPW 60
QY 61 DARPPAPSPFRQVSCHELVARYLQRLCERGANVLAFGFALLDARGSPPEAFTTSVR 120
DB 61 DARPPAPSPFRQVSCHELVARYLQRLCERGANVLAFGFALLDARGSPPEAFTTSVR 120
QY 121 SYLPTVTDLRGSGANGLLRRYGDVYLHLLARCLFVLVAPSCAYVCGSPPLYQLGA 180
DB 121 SYLPTVTDLRGSGANGLLRRYGDVYLHLLARCLFVLVAPSCAYVCGSPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLGCERAMNHSVREAGVPLGLPAPGARRGGSASRSLPLPKPRR 240
DB 181 ATQARPPPHASGPRRLGCERAMNHSVREAGVPLGLPAPGARRGGSASRSLPLPKPRR 240
QY 241 GAABEPRTVYGGGSAHFGTRGSPDRGFCVVSAPAPABEATSLGALSSTHSHPSVG 300
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QY 361 VEITFLGSRPWPCTPRRLPLPQRYWQMBLFLLELGNHAQCPYGLLTKHCEPLRAVT 420
DB 361 VEITFLGSRPWPCTPRRLPLPQRYWQMBLFLLELGNHAQCPYGLLTKHCEPLRAVT 420
QY 421 PAAVCARERKQGVAAPEEDTDPRLVOLLROHSSPMQVYGGVRACLARVLPGLMGS 480
DB 421 PAAVCARERKQGVAAPEEDTDPRLVOLLROHSSPMQVYGGVRACLARVLPGLMGS 480
QY 481 RHNERRPLRNTKKFISLGKHAKLSIQELTWKSVYDCAMLRSPGVGCVPAAEHRRLREI 540
DB 481 RHNERRPLRNTKKFISLGKHAKLSIQELTWKSVYDCAMLRSPGVGCVPAAEHRRLREI 540

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DB 481 RHNERRPLRNTKKFISLGKHAKLSIQELTWKSVYDCAMLRSPGVGCVPAAEHRRLREI 540
QY 541 LAKFLHMLMSYVVELLRSSFFVYVTEETFOKNRLEFFRYRBSVMSKLSIGIRQHLKRVQJRE 600
DB 541 LAKFLHMLMSYVVELLRSSFFVYVTEETFOKNRLEFFRYRBSVMSKLSIGIRQHLKRVQJRE 600
QY 601 LSEAVERQRREARPAILLTSRLRFLPKPDGLAPVIMMDVYVAGARTFRERKRERLTSRYKA 660
DB 601 LSEAVERQRREARPAILLTSRLRFLPKPDGLAPVIMMDVYVAGARTFRERKRERLTSRYKA 660
QY 661 LPSVLYNERRARPGLLGASVGLDIDHRAWRTFVLRYAQQPPPELYEVKVDVGAYDTI 720
DB 661 LPSVLYNERRARPGLLGASVGLDIDHRAWRTFVLRYAQQPPPELYEVKVDVGAYDTI 720
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DB 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAHGHVRAFKSHVSTLTDLQZYMQFVAHL 780
QY 781 QETSPLRDAVVEQSSSINEASSGLFDVFLRFMCHHAVIRIGKSYVCCGIPQGSILSTL 840
DB 781 QETSPLRDAVVEQSSSINEASSGLFDVFLRFMCHHAVIRIGKSYVCCGIPQGSILSTL 840
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DB 961 NRGFAGNNMRKLPGLVRLKXHSLELDOVNSIQVCTNITYKILLGAYEFHACVQLP 1020
QY 1021 FHOQVWKQPTFFLRISITSTASICYSILKAKNAGMSLGAKGAGPSPSAVQMLCHQAFIL 1080
DB 1021 FHOQVWKQPTFFLRISITSTASICYSILKAKNAGMSLGAKGAGPSPSAVQMLCHQAFIL 1080
QY 1081 KLTRRRTVYVPLGLSLRTAQQLSRKLPGLTTLTLEAANPALPSDFETIIL 1132
DB 1081 KLTRRRTVYVPLGLSLRTAQQLSRKLPGLTTLTLEAANPALPSDFETIIL 1132

RESULT 29
US-10-044-539-323
; Sequence 323, Application US/10044539
; Publication No. US2003010093A1
GENERAL INFORMATION:
  APPLICANT: Czech, Thomas R.
              Lingner, Joachim
              Nakamura, Toru
              Chapman, Karen B.
              Morin, Gregg B.
              Harley, Calvin
              Andrews, William H.
  TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
  THERAPEUTIC METHODS
  NUMBER OF SEQUENCES: 335
  CORRESPONDENCE ADDRESS:
    ADDRESSER: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, 8th floor
    CITY: San Francisco
    STATE: California
    COUNTRY: United States of America
    ZIP: 94111
  COMPUTER READABLE FORM:
    MEDIUM TYPE: floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/044,539
    FILING DATE: 11-Jan-2002

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FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ausenhus, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-00262005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 611:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1154 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1154
 OTHER INFORMATION: /note="fusion protein composed of hTERT protein sequence, vector sequences, the Myc epitope and His tag"
 SEQUENCE DESCRIPTION: SEQ ID NO: 611:
 US-10-325-810-611
 Query Match 99.8%; Score 5952; DB 14; Length 1154;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPAPRCRAVSLRLSHRYREVLPATFVRLGPGQWRLVORGDPAPAFRAIVACLVCM 60
 Db 1 MPAPRCRAVSLRLSHRYREVLPATFVRLGPGQWRLVORGDPAPAFRAIVACLVCM 60
 QY 61 DAPPAPAPSFROYSCIKELVAVYLQRLCERGAKNVLAFGFALLDARGGPPAFTTSVR 120
 Db 61 DAPPAPAPSFROYSCIKELVAVYLQRLCERGAKNVLAFGFALLDARGGPPAFTTSVR 120
 QY 121 SYLPNTVTDALRSGGAMGILLRRVGDVIVHLLARCLFTLVAPSCAYVCGSPYLQLA 180
 Db 121 SYLPNTVTDALRSGGAMGILLRRVGDVIVHLLARCLFTLVAPSCAYVCGSPYLQLA 180
 QY 181 ATOARPPHASPGRRLCGERAMNHSVREAGVPLGAPAGARRGGASRSLPLPKRPRR 240
 Db 181 ATOARPPHASPGRRLCGERAMNHSVREAGVPLGAPAGARRGGASRSLPLPKRPRR 240
 QY 241 GAAPPEPRITVGGGSAHAPGRTGPDRCGCVVSPAPPAEATSLGALSGTHSPSVG 300
 Db 241 GAAPPEPRITVGGGSAHAPGRTGPDRCGCVVSPAPPAEATSLGALSGTHSPSVG 300
 QY 301 ROHHAGPSTSRPPRPMDTCPPIYATKTFILYSSGDKQLRSPFLSSLRPLTGARRL 360
 Db 301 ROHHAGPSTSRPPRPMDTCPPIYATKTFILYSSGDKQLRSPFLSSLRPLTGARRL 360
 QY 361 VETIFLGRPMWPGTPRRLPLRFQRYWQMRPLFELIGNHAQCPYGVILKTHCPLRAAVT 420
 Db 361 VETIFLGRPMWPGTPRRLPLRFQRYWQMRPLFELIGNHAQCPYGVILKTHCPLRAAVT 420
 QY 421 PAGVCAAREKQGSVAAPBEEDTDPRRLVQLLRHSSPWQVYGVFVRACLRLPLPGMG 480

Db 421 PAAGVCAAREKQGSVAAPBEEDTDPRRLVQLLRHSSPWQVYGVFVRACLRLPLPGMG 480
 QY 481 RHNERFRLNTKKFSLGKHAKLSTOELTWKMSVRDCAMLRSPGVGCVPAAREHRLREI 540
 Db 481 RHNERFRLNTKKFSLGKHAKLSTOELTWKMSVRDCAMLRSPGVGCVPAAREHRLREI 540
 QY 541 LAKFLHMLMSYVVVELLSRFFVYETTFQXKRLFFPRPSVMSKLQSIGIRQHLKRVQIRE 600
 Db 541 LAKFLHMLMSYVVVELLSRFFVYETTFQXKRLFFPRPSVMSKLQSIGIRQHLKRVQIRE 600
 QY 601 LSEAEVRQHRARPALLTSRLRFTPKPGCLRPITNMDVVGAAFTFRREKRELTSPYKA 660
 Db 601 LSEAEVRQHRARPALLTSRLRFTPKPGCLRPITNMDVVGAAFTFRREKRELTSPYKA 660
 QY 661 LFSVLYNERARPPGLGASVGLDDIRHAWRTFYLRYAQQPPPELYFVKYDVTGAYDTI 720
 Db 661 LFSVLYNERARPPGLGASVGLDDIRHAWRTFYLRYAQQPPPELYFVKYDVTGAYDTI 720
 QY 721 PQDLTEVIASTIKQNTYCYRRAVAVOKAHGVRKAFKSHVSTLTDLOPYMQFVAHL 780
 Db 721 PQDLTEVIASTIKQNTYCYRRAVAVOKAHGVRKAFKSHVSTLTDLOPYMQFVAHL 780
 QY 781 QETSPLRDAVYIEGSSSLNEASSGLFDVFLRFMGCHAVRIRGKSYVQCQGIPOGSIISTL 840
 Db 781 QETSPLRDAVYIEGSSSLNEASSGLFDVFLRFMGCHAVRIRGKSYVQCQGIPOGSIISTL 840
 QY 841 LCSLCYGMENKLPAGIRRDGLLRVDDPLVTPHLLTHANTPLRTLVGVPBYGCVNL 900
 Db 841 LCSLCYGMENKLPAGIRRDGLLRVDDPLVTPHLLTHANTPLRTLVGVPBYGCVNL 900
 QY 901 RKTVPNFEVEDEALGGTAFVQMPAHGLFPWCGILLDPRTLEVOSDYASTSRASVTF 960
 Db 901 RKTVPNFEVEDEALGGTAFVQMPAHGLFPWCGILLDPRTLEVOSDYASTSRASVTF 960
 QY 961 NRGFGAGNMRRKLFVGLRLKCHSLFDLDQVNSIQVCTNIIYKILLQAYEFHACVQLP 1020
 Db 961 NRGFGAGNMRRKLFVGLRLKCHSLFDLDQVNSIQVCTNIIYKILLQAYEFHACVQLP 1020
 QY 1021 FHQQWKNKPTFFPLRISTTASLCYSILKAKNAGSLGKGAAGPLPSAVWMLQDAVLL 1080
 Db 1021 FHQQWKNKPTFFPLRISTTASLCYSILKAKNAGSLGKGAAGPLPSAVWMLQDAVLL 1080
 QY 1081 KLTRHRTVYVPLGSLRTAQQLSRKLPGLTTLTALEAANPALPSDFETIIL 1132
 Db 1081 KLTRHRTVYVPLGSLRTAQQLSRKLPGLTTLTALEAANPALPSDFETIIL 1132
 RESULT 31
 US-10-877-124-611
 ; Sequence 611, Application US/10877124
 ; Publication No. US20040242529A1
 GENERAL INFORMATION:
 APPLICANT: Czech, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Hatley, Calvin B.
 ; Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,124

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999

APPLICATION NUMBER: 08/974,549

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-May-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-Oct-1997

APPLICATION NUMBER: WO PCT/US97/17865

FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

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INFORMATION FOR SEQ ID NO: 611:

SEQUENCE CHARACTERISTICS:

LENGTH: 1154 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..1154

OTHER INFORMATION: /note= "fusion protein composed of hTERT protein sequence, vector sequences, the Myc epitope and His6 tag"

SEQUENCE DESCRIPTION: SEQ ID NO: 611:

US-10-877-124-611

Query Match 99.8%; Score 5952; DB 17; Length 1154;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRARRCRAVRSLSHREVLPLATFVRRLQPGQWRVLVQGDPAFAFALVAQCLVCPW 60

DB 1 MRAPRCRAVRSLSHREVLPLATFVRRLQPGQWRVLVQGDPAFAFALVAQCLVCPW 60

QY 61 DARPPAPAFRQVSCIKELVARVLQRLCERGAKNVLAFFGALLDGAAGCPPEAFTTSVR 120

DB 61 DARPPAPAFRQVSCIKELVARVLQRLCERGAKNVLAFFGALLDGAAGCPPEAFTTSVR 120

QY 121 STLPNTVTDALFGSGAGWGLLRVDDVVLVHLARCAFLVVAISCAVQVCPPLVQLGA 180

DB 121 STLPNTVTDALFGSGAGWGLLRVDDVVLVHLARCAFLVVAISCAVQVCPPLVQLGA 180

QY 181 ATQARPPPIASGPRRLGGERAMNHSVREAGVPLGLPAGARRRGSASRSLP.PKSPRR 240

DB 181 ATQARPPPIASGPRRLGGERAMNHSVREAGVPLGLPAGARRRGSASRSLP.PKSPRR 240

QY 241 GAAPPERTPVGGQSWAHPGRTGRGSDRGFCVSPAPAEATSLGALSSTRHSBVG 300

DB 241 GAAPPERTPVGGQSWAHPGRTGRGSDRGFCVSPAPAEATSLGALSSTRHSBVG 300

QY 301 RQHAGBPSTSRPPRPMDTPCPVVAETKHPLYSSGDKQLRPSFLSSRLSGRLGARL 360

DB 301 RQHAGBPSTSRPPRPMDTPCPVVAETKHPLYSSGDKQLRPSFLSSRLSGRLGARL 360

QY 361 VETIFIGSRPMPGTPRRLPLRQRYOMRPLFELIGNHACCPGVLLKTCPLRAAYT 420

DB 361 VETIFIGSRPMPGTPRRLPLRQRYOMRPLFELIGNHACCPGVLLKTCPLRAAYT 420

QY 421 PAAGVAREXPQGSVAAPBEDTDPRLVOLLROHSPMVQYGFVACLRLLVPGLMGS 480

DB 421 PAAGVAREXPQGSVAAPBEDTDPRLVOLLROHSPMVQYGFVACLRLLVPGLMGS 480

QY 481 RHNERFLRNTKFKFISLGAKLSTLOELTWKSVPCALRRSPGVCVPAEHLRRETI 540

DB 481 RHNERFLRNTKFKFISLGAKLSTLOELTWKSVPCALRRSPGVCVPAEHLRRETI 540

QY 541 LAPELWMSVYVVELRSPFFVYETTFQKNLFFRPSWMSKLSIGIRQLKRYLRE 600

DB 541 LAPELWMSVYVVELRSPFFVYETTFQKNLFFRPSWMSKLSIGIRQLKRYLRE 600

QY 601 LSAEVRQREARFALLTSRFLRIPKPDGLRPIVMNDYVVGARTRRERARLTSRYVA 660

DB 601 LSAEVRQREARFALLTSRFLRIPKPDGLRPIVMNDYVVGARTRRERARLTSRYVA 660

QY 661 LFSVLNVERARPRGLGASVLAGDDIHRAMRFVLRAQDPPELYFVKVDTGAYDTI 720

DB 661 LFSVLNVERARPRGLGASVLAGDDIHRAMRFVLRAQDPPELYFVKVDTGAYDTI 720

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DB 721 PQRLTEVIASIIKPNNTYCVRRYAVQKAHGVAKFHSVSTLTDIOPYMRQFVAL 780

QY 781 QETSPLRDVAIVHSSSLNEASGLFDVLRPMCHAAVIRKSYVQCGIGQSLSTL 840

DB 781 QETSPLRDVAIVHSSSLNEASGLFDVLRPMCHAAVIRKSYVQCGIGQSLSTL 840

QY 841 LGSICYGDMENKLFAGIRRDGLLRVDDPLVTPHLTAKTFLRLTVAGVEYGVNL 900

DB 841 LGSICYGDMENKLFAGIRRDGLLRVDDPLVTPHLTAKTFLRLTVAGVEYGVNL 900

QY 901 RKTIVNFPVEDEALGGAFAVQMPAHGLFPWCGLLDTRLLEVQSDYSASIASATYF 960

DB 901 RKTIVNFPVEDEALGGAFAVQMPAHGLFPWCGLLDTRLLEVQSDYSASIASATYF 960

QY 961 NRGFKAGRMNRKLFVLRKCHSLFLDQVNSLQVCTNIYKILLIQAYRFACVQLP 1020

DB 961 NRGFKAGRMNRKLFVLRKCHSLFLDQVNSLQVCTNIYKILLIQAYRFACVQLP 1020

QY 1021 FHOQWKNPTFFLRVISDTASLCTSLKAKNAGMSLGAAGAAGPLPSEAVQMLCHQAFLL 1080

DB 1021 FHOQWKNPTFFLRVISDTASLCTSLKAKNAGMSLGAAGAAGPLPSEAVQMLCHQAFLL 1080

QY 1081 KLTRHRVTYVPLIGSLRTAQTOLSRKLPGLTTLTALEAANPALPSPDKTILD 1132

DB 1081 KLTRHRVTYVPLIGSLRTAQTOLSRKLPGLTTLTALEAANPALPSPDKTILD 1132

RESULT 32

US-10-877-022-611

Sequence 611, Application US/10877022

Publication No. US20040247613A1

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Martin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
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 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/677,022
 FILING DATE: 24-Jun-2004
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/432,503
 FILING DATE: 02-Nov-1999
 APPLICATION NUMBER: 08/974,549
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-May-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-Oct-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 611:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1154 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1154
 OTHER INFORMATION: /note= "fusion protein composed of hTET
 protein sequence, vector sequences, the
 Myc epitope and His6 tag"
 SEQUENCE DESCRIPTION: SEQ ID NO: 611:
 US-10-877-022-611

Query Match 99.8%; Score 5952; DB 17; Length 1154;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPRAAPCAVSLRSHREVLPATFVRRLPGQWRLVORGDPAAFRALVAQCLVCPW 60
 Db 1 MPRAAPCAVSLRSHREVLPATFVRRLPGQWRLVORGDPAAFRALVAQCLVCPW 60

Qy 61 DARPPAPSTRQVSCLEKELVARVLQRCERGAQNVLAFGFALLDGRGSPPEAFITTSVR 120
 Db 61 DARPPAPSTRQVSCLEKELVARVLQRCERGAQNVLAFGFALLDGRGSPPEAFITTSVR 120

121 SYLPTVTDALRGSGAMGLLRVGDVVLHLLARCALFLVAPSCAYQVCGPFLYOLGA 180
 121 SYLPTVTDALRGSGAMGLLRVGDVVLHLLARCALFLVAPSCAYQVCGPFLYOLGA 180

Qy 181 ATOARPPPHASGPPRRRLGCEPAMNHSVREAGVPGLPAFGARRRGSSASSLPLPKPRR 240
 Db 181 ATOARPPPHASGPPRRRLGCEPAMNHSVREAGVPGLPAFGARRRGSSASSLPLPKPRR 240

Qy 241 GAAPPEPTPVQGSMAHPGRTGSDRGFCVSPAPAEBAATSLLEGALSTGRSHSVG 300
 Db 241 GAAPPEPTPVQGSMAHPGRTGSDRGFCVSPAPAEBAATSLLEGALSTGRSHSVG 300

Qy 301 RQHHAGPSTSRPPRPMDTCCPVYAETKHELYSGDXEQLRPSFLLSLRPSLTGARL 360
 Db 301 RQHHAGPSTSRPPRPMDTCCPVYAETKHELYSGDXEQLRPSFLLSLRPSLTGARL 360

Qy 361 VETIFLGSRPWMPGTPRRLLPRLPQRYQMRPLFELLGNHACQCYVLKTHGCLRAVT 420
 Db 361 VETIFLGSRPWMPGTPRRLLPRLPQRYQMRPLFELLGNHACQCYVLKTHGCLRAVT 420

Qy 421 PAAGVCAREKPOGSAVAPEEEDTPRRLYQLRQHSBWCYVGVFVACLRLLVPGJLMS 480
 Db 421 PAAGVCAREKPOGSAVAPEEEDTPRRLYQLRQHSBWCYVGVFVACLRLLVPGJLMS 480

Qy 481 RHNERFLRNTKPFISLGKHAKLISLOETWMSVSDCAMELRSPGVGCVPAEHRLEBEI 540
 Db 481 RHNERFLRNTKPFISLGKHAKLISLOETWMSVSDCAMELRSPGVGCVPAEHRLEBEI 540

Qy 541 LAKELHMLMSVYVELLSFFVYETTPQKNRLFFYRPSVMSKQSIGIRQHLRVOLRE 600
 Db 541 LAKELHMLMSVYVELLSFFVYETTPQKNRLFFYRPSVMSKQSIGIRQHLRVOLRE 600

Qy 601 LSEAEVRQREARPALTSRLRFIPKPDGLRPIVMNDVVGARTFRREKRAERLTSRYKA 660
 Db 601 LSEAEVRQREARPALTSRLRFIPKPDGLRPIVMNDVVGARTFRREKRAERLTSRYKA 660

Qy 661 LFSVTNVRARRPGLLGASVGLDIIHRAMRTVILRVAAOBBPEPLVAVKIDVGAAYTI 720
 Db 661 LFSVTNVRARRPGLLGASVGLDIIHRAMRTVILRVAAOBBPEPLVAVKIDVGAAYTI 720

Qy 721 PODRLTEVYASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLIDLPYMRQFVAHL 780
 Db 721 PODRLTEVYASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLIDLPYMRQFVAHL 780

Qy 781 QETSPLRDAVITEGSSSLNEASSGLFDVFLRPMCHAVRIKGSVVOQGIPOGSLSTL 840
 Db 781 QETSPLRDAVITEGSSSLNEASSGLFDVFLRPMCHAVRIKGSVVOQGIPOGSLSTL 840

Qy 841 LCSLCYGMENKLPFAGIRRDGLRLVDDFLVTPHLTHAKTFRTLVGPEYECVNVL 900
 Db 841 LCSLCYGMENKLPFAGIRRDGLRLVDDFLVTPHLTHAKTFRTLVGPEYECVNVL 900

Qy 901 RKTIVNFPVEDEALGTAFFVQMPAHGLFPWCGLLIDRTLLEQSSYSYARSISASLTF 960
 Db 901 RKTIVNFPVEDEALGTAFFVQMPAHGLFPWCGLLIDRTLLEQSSYSYARSISASLTF 960

Qy 961 NNGFKAGNMRKLGAVRIKCHSLFDLQVNSLCTVCTNIYKILLDAYRHAQCLDP 1020
 Db 961 NNGFKAGNMRKLGAVRIKCHSLFDLQVNSLCTVCTNIYKILLDAYRHAQCLDP 1020

Qy 1021 FHOQVWKXNPTFLRVIISDTASLCVSLKAKNAGMSLGAKGAAGPLPSBAVQMLCQAEDL 1080
 Db 1021 FHOQVWKXNPTFLRVIISDTASLCVSLKAKNAGMSLGAKGAAGPLPSBAVQMLCQAEDL 1080

Qy 1081 KLTRHRVTVVPLLSLRTAQTOLSKRLPGTTLTALEAANPALPSDFKTLID 1132
 Db 1081 KLTRHRVTVVPLLSLRTAQTOLSKRLPGTTLTALEAANPALPSDFKTLID 1132

Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 325:
US-10-044-692-325
Query Match 99.8%; Score 5952; DB 14; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPBARCRAVSLRSHRYEVLPLATFVRRLGPGQWPLVORGDPAAARALVAOQLVCVPM 60
DB 58 MPBARCRAVSLRSHRYEVLPLATFVRRLGPGQWPLVORGDPAAARALVAOQLVCVPM 117
QY 61 DARPPAPSRFQVSCLELVARVLQRLCERGANVLAFGFALDGAAGGPEAFTTSVR 120
DB 118 DARPPAPSRFQVSCLELVARVLQRLCERGANVLAFGFALDGAAGGPEAFTTSVR 177
QY 121 SYLEVTVDALRGSGAMGLLRVYDDVVLHLLARCALFVIVASCAVYVCGPPLYLQGA 180
DB 178 SYLEVTVDALRGSGAMGLLRVYDDVVLHLLARCALFVIVASCAVYVCGPPLYLQGA 237

QY 181 ATQARPPPHASGPRRRIGCERAMNHSVREAGVPLGAPAGARRRGSASRLPLPKRPR 240
DB 238 ATQARPPPHASGPRRRIGCERAMNHSVREAGVPLGAPAGARRRGSASRLPLPKRPR 297
QY 241 GAAPERTPVGQSMNHPARTGSPRGCVVSPAPAEATSLGALSGTHSPVSG 300
DB 298 GAAPERTPVGQSMNHPARTGSPRGCVVSPAPAEATSLGALSGTHSPVSG 357
QY 301 ROHAGPSTSRPPRPDPCPPVYATKFLVYSSGDKQRLSPFLSSLRPLTGARRL 360
DB 358 ROHAGPSTSRPPRPDPCPPVYATKFLVYSSGDKQRLSPFLSSLRPLTGARRL 417
QY 361 VETIFLGRPMWMTGTPRRLPLPQRYWQKRLPLLELLGNHAQCPYVLLKTHQPLAAVT 420
DB 418 VETIFLGRPMWMTGTPRRLPLPQRYWQKRLPLLELLGNHAQCPYVLLKTHQPLAAVT 477
QY 421 PAAGVCAERKPGQSVAAPEEEDTDPRRLVOLLRQHSPPQVYGFVACLRRLVPLMG 480
DB 478 PAAGVCAERKPGQSVAAPEEEDTDPRRLVOLLRQHSPPQVYGFVACLRRLVPLMG 537
QY 481 RHNERRRLNTKTKFISLGKAKLSLOELTKWSVRDCAMLRSPGVGVPAAEHRIREI 540
DB 538 RHNERRRLNTKTKFISLGKAKLSLOELTKWSVRDCAMLRSPGVGVPAAEHRIREI 597
QY 541 LAKEFLHMSVYVVELRSPFYVTEETTPQKNRLFEPYRSPWSKLSIGIRHLKRYQLRE 600
DB 598 LAKEFLHMSVYVVELRSPFYVTEETTPQKNRLFEPYRSPWSKLSIGIRHLKRYQLRE 657
QY 601 LSEAVERQREARPAALTSRLRPIPKPDGLRPIVMDVYVAGARTPREKRAERLTSRYKA 660
DB 658 LSEAVERQREARPAALTSRLRPIPKPDGLRPIVMDVYVAGARTPREKRAERLTSRYKA 717
QY 661 LFSVLNTERARRPGLGASVLTGIDITHRAMRFVLRVRAQDPPELYPFKVVNTGAYDTI 720
DB 718 LFSVLNTERARRPGLGASVLTGIDITHRAMRFVLRVRAQDPPELYPFKVVNTGAYDTI 777
QY 721 PODRLTEVLAIIKPPONTYCVARAYAVQCAAGHAKAFKSHVSTLTLDQPYMRQFVAHL 780
DB 778 PODRLTEVLAIIKPPONTYCVARAYAVQCAAGHAKAFKSHVSTLTLDQPYMRQFVAHL 837
QY 781 QETSPLRDAVYIEQSSLSNEASSGLFDVFLRMCHNAVIRKSYVCCGILQSSILSTL 840
DB 838 QETSPLRDAVYIEQSSLSNEASSGLFDVFLRMCHNAVIRKSYVCCGILQSSILSTL 897
QY 841 LCSLCYGDMEKMLFAGIRRDGLLRLVDDFLVTPHLTHAKFTLTVKGVDEYGCYNL 900
DB 898 LCSLCYGDMEKMLFAGIRRDGLLRLVDDFLVTPHLTHAKFTLTVKGVDEYGCYNL 957
QY 901 RKTIVNFPVEDEALGSTAFVQMPAHGLFPWCGLLIDRTLLEVQSDYSYARTSIRASVTF 960
DB 958 RKTIVNFPVEDEALGSTAFVQMPAHGLFPWCGLLIDRTLLEVQSDYSYARTSIRASVTF 1017
QY 961 NRGFKAGRMRRKLFQVLRKCHSLFLDQVNSLTQVCTNIYKILLQAYRPHAQVQLP 1020
DB 1018 NRGFKAGRMRRKLFQVLRKCHSLFLDQVNSLTQVCTNIYKILLQAYRPHAQVQLP 1077
QY 1021 FHQQWKNPTFFLRVYISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAEFL 1080
DB 1078 FHQQWKNPTFFLRVYISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAEFL 1137
QY 1081 KLTRHRYTVYVPLLSLRTAQTLQSLKRGTTTLTALEAANPLPBDFTTIID 1132
DB 1138 KLTRHRYTVYVPLLSLRTAQTLQSLKRGTTTLTALEAANPLPBDFTTIID 1189

RESULT 34
US-10-044-539-325
Sequence 325, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim

1 Nakamura, Toru
2 Chapman, Karen B.
3 Morin, Gregg B.
4 Harley, Calvin
5 Andrews, William H.
6 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
7 THERAPEUTIC METHODS
8 NUMBER OF SEQUENCES: 335
9 CORRESPONDENCE ADDRESSES:
10 ADDRESSEE: Townsend and Townsend and Crew LLP
11 STREET: Two Embarcadero Center, 8th Floor
12 CITY: San Francisco
13 STATE: California
14 COUNTRY: United States of America
15 ZIP: 94111
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/10/044,539
23 FILING DATE: 11-Jan-2002
24 CLASSIFICATION: 435
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 08/912,951
27 FILING DATE: <Unknown>
28 APPLICATION NUMBER: US 08/854,050
29 FILING DATE: 09-MAY-1997
30 APPLICATION NUMBER: US 08/851,843
31 FILING DATE: 06-MAY-1997
32 APPLICATION NUMBER: US 08/846,017
33 FILING DATE: 25-APR-1997
34 APPLICATION NUMBER: US 08/844,419
35 FILING DATE: 18-APR-1997
36 APPLICATION NUMBER: US 08/724,643
37 FILING DATE: 01-OCT-1996
38 ATTORNEY/AGENT INFORMATION:
39 NAME: Apple, Randolph T.
40 REGISTRATION NUMBER: 36,429
41 REFERENCE/DOCKET NUMBER: 015389-002600US
42 TELECOMMUNICATION INFORMATION:
43 TELEPHONE: (415) 576-0200
44 TELEFAX: (415) 576-0300
45 INFORMATION FOR SEQ ID NO: 325:
46 SEQUENCE CHARACTERISTICS:
47 LENGTH: 1189 amino acids
48 TYPE: amino acid
49 STRANDEDNESS: <Unknown>
50 TOPOLOGY: linear
51 MOLECULE TYPE: protein
52 SEQUENCE DESCRIPTION: SEQ ID NO: 325:
53 US-10-044-539-325
54
55 Query Match 99.8%; Score 5952; DB 14; Length 1189;
56 Best Local Similarity 99.8%; Pred. No. 0;
57 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

241 GAAPPERTPVGGSWAHGRTGSPDRGFCVVS PAR PAEBATSLGALSGTRHSPSVG 300
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358 ROHAGPSTSRPRPMDTPCPVYAEIKFELYSGGXEQULRPSFLLSRLPGARL 417
361 VETTLGSRPMPGTPRRLPRLPORVYOMRLEFELLGNHACQCYGVLLKTHCLRAVT 420
418 VETTLGSRPMPGTPRRLPRLPORVYOMRLEFELLGNHACQCYGVLLKTHCLRAVT 477
421 PAAGVCAEKPOGSAAPAEEDTPRRLVOLLRQHSFPMQYGVFVACRLRVPGLMGS 480
478 PAAGVCAEKPOGSAAPAEEDTPRRLVOLLRQHSFPMQYGVFVACRLRVPGLMGS 537
481 RHNERFLRNTKFTSLGKHAKLSLQELTWMSYRDCAMLRSPGVGCPAAEHLRLEEI 540
538 RHNERFLRNTKFTSLGKHAKLSLQELTWMSYRDCAMLRSPGVGCPAAEHLRLEEI 597
541 LAKELHWMMSVYVVELLSFFVYETTFQKRLFFVPSVSKLQSIGIRHLLKRVQRE 600
598 LAKELHWMMSVYVVELLSFFVYETTFQKRLFFVPSVSKLQSIGIRHLLKRVQRE 657
601 LSEAEVRQREARPALTLTSLRLETPKPDGLRPIVMMDVVGARTFRREKRAERLTSRYKA 660
658 LSEAEVRQREARPALTLTSLRLETPKPDGLRPIVMMDVVGARTFRREKRAERLTSRYKA 717
661 LFSVINYRARRPGLIGSVGLDIDIRAKMTFVLKRAQCPPELVKVDVGAQDTI 720
718 LFSVINYRARRPGLIGSVGLDIDIRAKMTFVLKRAQCPPELVKVDVGAQDTI 777
721 PODRLTEVIASIKPONTYCVRRYAVVQKAHGVKAKFHSVSTLIDLPYKQFVAHL 780
778 PODRLTEVIASIKPONTYCVRRYAVVQKAHGVKAKFHSVSTLIDLPYKQFVAHL 837
781 QETSPLRDAVYIEQSSSINEASSGLFDVFLRPMCHAVRIGKSVYCCGIPQGSII STL 840
838 QETSPLRDAVYIEQSSSINEASSGLFDVFLRPMCHAVRIGKSVYCCGIPQGSII STL 897
841 LCLCYGMENKLPFGIRRDGLLRVDPLVPHLHAKTPTLTVRGVPEGVNVL 900
898 LCLCYGMENKLPFGIRRDGLLRVDPLVPHLHAKTPTLTVRGVPEGVNVL 957
901 KRTVNFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQDSYSYARTSIRASLTF 960
958 KRTVNFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQDSYSYARTSIRASLTF 1017
961 NRGFAKGNMRKLPFGVLRKCHSLFDLQVNSLOTVTNLYKILLQAYFHCVQLDP 1020
1018 NRGFAKGNMRKLPFGVLRKCHSLFDLQVNSLOTVTNLYKILLQAYFHCVQLDP 1077
1021 FHQQWKAJPTFLKRIYSDTASLCYSILKAKNAGMSLGAKGAGPLPSBAVOMLCHQAEFL 1080
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1081 KLTRHRTVYVPLLSLRTAQOLSRKLPGLTTLTALAANPALPBDFTIID 1132
1138 KLTRHRTVYVPLLSLRTAQOLSRKLPGLTTLTALAANPALPBDFTIID 1189

RESULT 35
US-10-325-810-613
Sequence 613, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.

Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 613
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Townsend and Townsend and Crew LLP
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/325,810
 FILING DATE: 20-Dec-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,181
 FILING DATE: 29-Sep-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-Oct-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-May-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: WO PCT/US97/117885
 FILING DATE: 01-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ausenius, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 613:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1189 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1189
 OTHER INFORMATION: /note= "fusion protein composed of
 hTERT signal sequence and full length
 hTERT protein"
 SEQUENCE DESCRIPTION: SEQ ID NO: 613:
 US-10-325-810-613
 Query Match 99.8%; Score 5952; DB 14; Length 1189;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MPRARCAVRSLLSHREVLPATFVRRLGPGCMRLVORGDDPAFAFALVAQCLVCYVPW 60
 DB 58 MPRARCAVRSLLSHREVLPATFVRRLGPGCMRLVORGDDPAFAFALVAQCLVCYVPW 117
 QY 61 DARPPAAPSPROVSCLELVARVLORLCERGAKNVLAFGFALLDGAAGGPPFAFTTSVR 120

Db 118 DARPPAAPSPROVSCLELVARVLORLCERGAKNVLAFGFALLDGAAGGPPFAFTTSVR 177
 QY 121 SYLPNTVTDALRSGAGMLLRVGDDVLYHLARCALFLVAPSCAYOCCGPLYQLGA 180
 Db 178 SYLPNTVTDALRSGAGMLLRVGDDVLYHLARCALFLVAPSCAYOCCGPLYQLGA 237
 QY 181 ATOARPPHAGSPRRRLGCERANNSVREAGVPLGAPARRRGSASRLPLPRPR 240
 Db 238 ATOARPPHAGSPRRRLGCERANNSVREAGVPLGAPARRRGSASRLPLPRPR 297
 QY 241 GAAPERTPTVGGSNMHPGRTGPGSDRGCVVSAPRAPEATSLGALSGTSHSPSG 300
 Db 298 GAAPERTPTVGGSNMHPGRTGPGSDRGCVVSAPRAPEATSLGALSGTSHSPSG 357
 QY 301 ROHHAGPPTSRPPRPMDTCCPVVAETKFLVSSGDKQLRPSFLSSRLPSLTGARLT 360
 Db 358 ROHHAGPPTSRPPRPMDTCCPVVAETKFLVSSGDKQLRPSFLSSRLPSLTGARLT 417
 QY 361 VETIFLGSRRPMWGTPTPLRPLPQRYWQMPLELLGNHAQCPYVLLKTHCPLRAAT 420
 Db 418 VETIFLGSRRPMWGTPTPLRPLPQRYWQMPLELLGNHAQCPYVLLKTHCPLRAAT 477
 QY 421 PAAGVCAERKPGQSVAPAEEDTDPRLVQLRQSSPMQVGYFVACLRRLVPPGLMS 480
 Db 478 PAAGVCAERKPGQSVAPAEEDTDPRLVQLRQSSPMQVGYFVACLRRLVPPGLMS 537
 QY 481 RHNERPRLNTKFFISLGHAKLSLOELTWKMSVRDCAMLRSPGYCVPAAEHRLREI 540
 Db 538 RHNERPRLNTKFFISLGHAKLSLOELTWKMSVRDCAMLRSPGYCVPAAEHRLREI 597
 QY 541 LAKEFLHMSVYVVELLRSPFYETTPQKNRLFPRPVMWSLQSIGRQLKRYQLRE 600
 Db 598 LAKEFLHMSVYVVELLRSPFYETTPQKNRLFPRPVMWSLQSIGRQLKRYQLRE 657
 QY 601 LSEAVERQHEARPAALLTSRLRPIPKDGLRPIVMNDVYVAGARTPREREARLTSRYKA 660
 Db 658 LSEAVERQHEARPAALLTSRLRPIPKDGLRPIVMNDVYVAGARTPREREARLTSRYKA 717
 QY 661 LFSVLNVERARRPGLLGASVGLGDDIHRAMRFVLRVADDPPELRYFKVAVTGAIDTI 720
 Db 718 LFSVLNVERARRPGLLGASVGLGDDIHRAMRFVLRVADDPPELRYFKVAVTGAIDTI 777
 QY 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAGHVRKAKSVSTLTDLPYMRQFVAHL 780
 Db 778 PODRLTEVIASIIKPNQTYCVRRYAVVQKAGHVRKAKSVSTLTDLPYMRQFVAHL 837
 QY 781 QETSPLRDAVITPOSSSLNEASSGLFDVFLRMCHAVIRKGSYVQCGIFQGSILSTL 840
 Db 838 QETSPLRDAVITPOSSSLNEASSGLFDVFLRMCHAVIRKGSYVQCGIFQGSILSTL 897
 QY 841 LGSILCYGDMENKLEAGIRRDGILLRLVDDPFLVTPHLLTAKFTLTLVAGVEYGCVMIL 900
 Db 898 LGSILCYGDMENKLEAGIRRDGILLRLVDDPFLVTPHLLTAKFTLTLVAGVEYGCVMIL 957
 QY 901 RKTVMNFPVEDEALGTAIVQMPAHGLFPWCGLLDTRILEVQSDYSSTARSISASVTF 960
 Db 958 RKTVMNFPVEDEALGTAIVQMPAHGLFPWCGLLDTRILEVQSDYSSTARSISASVTF 1017
 QY 961 NRGFKAGRMRRRLFGVLRKLKCHSLFLDQVANSLOTCVNIYKILLLOAYRHACVLOLP 1020
 Db 1018 NRGFKAGRMRRRLFGVLRKLKCHSLFLDQVANSLOTCVNIYKILLLOAYRHACVLOLP 1077
 QY 1081 KLTRHRTVTVPLIGSLRTAOTQSLRCLPCTTLTALAAANPLPSPDFKTIID 1132
 Db 1138 KLTRHRTVTVPLIGSLRTAOTQSLRCLPCTTLTALAAANPLPSPDFKTIID 1189

RESULT 36
 US-10-877-124-613

Sequence 613, Application US/10877.124
 Publication No. US2004024529A1
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Hartley, Calvin B.
 Andrews, William H.
 TITLE OF INVENTION: Human telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/877,124
 FILING DATE: 24-Jun-2004
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/432,503
 FILING DATE: 02-Nov-1998
 APPLICATION NUMBER: 08/974,549
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-May-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-Aug-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-Oct-1997
 APPLICATION NUMBER: WO PCT/US97/17865
 FILING DATE: 01-Oct-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 613:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1189 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1189
 OTHER INFORMATION: /note="fusion protein composed of
 melittin signal sequence and full length
 hTERT protein"
 SEQUENCE DESCRIPTION: SEQ ID NO: 613:
 US-10-877-124-613

Query Match 99.8%; Score 5952; DB 17; Length 1189;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db	58	MPRAPRCRAVNSLIRSHREVLPATFYRLIGPGCNMLVQGDPAARALVAQCLVCVPM	117
Qy	61	DARPPAPSPFQVSCLELVARVLQRCERGANVLAFGALDGAAGSPPEAFTTSVR	120
Db	118	DARPPAPSPFQVSCLELVARVLQRCERGANVLAFGALDGAAGSPPEAFTTSVR	177
Qy	121	SYLPNTVTDALRGSGAMGLLRVYDDVYLHARLCALEVLVAPSCAYQVCGPPLYLQGA	180
Db	178	SYLPNTVTDALRGSGAMGLLRVYDDVYLHARLCALEVLVAPSCAYQVCGPPLYLQGA	237
Qy	181	ATQAPPPHAGSPRRRLGCEBAMNSVDEAGVPLGLPAGARRGSGASRLPLPKAPRR	240
Db	238	ATQAPPPHAGSPRRRLGCEBAMNSVDEAGVPLGLPAGARRGSGASRLPLPKAPRR	297
Qy	241	GAAPSPERTPVQGGSWAHPRGTRGSDRGFCVSPAPPAEATSLEGALSGTRSHSVG	300
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Qy	361	VETIFLGRPMWPGTFRRLPRLPORWQMRPLFELIGNHACCPGYVLTKHCPLEAAVT	420
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Qy	421	PAAGVCAEKKPGQSVAAPEEDTDRLLVOLLRQHSWQYGYVYACLRLLVPPGLMS	480
Db	478	PAAGVCAEKKPGQSVAAPEEDTDRLLVOLLRQHSWQYGYVYACLRLLVPPGLMS	537
Qy	481	RNERRPFRNTKFFSLGKHAKLSTQELTWKMSVDCMLRSPGVGCVPAEHRLESEI	540
Db	538	RNERRPFRNTKFFSLGKHAKLSTQELTWKMSVDCMLRSPGVGCVPAEHRLESEI	597
Qy	541	LAKFLHMLMSYVVLRSFFVYETTFQKNRLFYRPSWSKLSQISIRQHLKRVQURE	600
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Qy	601	ISEAEVRQREARPPALTLSTRLEFIKPDGLRPIVMQDVVGARTTRRKRERLTSRYKA	660
Db	658	ISEAEVRQREARPPALTLSTRLEFIKPDGLRPIVMQDVVGARTTRRKRERLTSRYKA	717
Qy	661	LFSVINYERARPPGLLGASVGLDDIHRAMRTFVLRAADPPPELVYKVDVTGAYDTI	720
Db	718	LFSVINYERARPPGLLGASVGLDDIHRAMRTFVLRAADPPPELVYKVDVTGAYDTI	777
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Qy	781	QETSPLRDAVVEQSSSLNEASGAFDYFLRMCCHAVRIRGKSVYQCGIFQGSILSTL	840
Db	838	QETSPLRDAVVEQSSSLNEASGAFDYFLRMCCHAVRIRGKSVYQCGIFQGSILSTL	897
Qy	841	LCSLCYGDMENKLPAGIRRDGLLRLVDDFLVTLVTHLTHAKTFLRTLVGVEYCVNLT	900
Db	898	LCSLCYGDMENKLPAGIRRDGLLRLVDDFLVTLVTHLTHAKTFLRTLVGVEYCVNLT	957
Qy	901	RKTVMNPFVEDALGGLTAFCVMEAHGLFPMCGLLDRTLEQSSYSSARSTISAVTF	960
Db	958	RKTVMNPFVEDALGGLTAFCVMEAHGLFPMCGLLDRTLEQSSYSSARSTISAVTF	1017
Qy	961	NRGFAGRMRRKRLGVLRKCHSLFDLQVNSLQVCTNIIYKILLQAYRFHACVQLP	1020
Db	1018	NRGFAGRMRRKRLGVLRKCHSLFDLQVNSLQVCTNIIYKILLQAYRFHACVQLP	1077

QY 1021 FHQVWKNPTEPFRVSDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVQWLCQATLL 1080
Db 1078 FHQVWKNPTEPFRVSDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVQWLCQATLL 1137
QY 1081 KLTRHVTVPPLGSLRTAQTQSRKLPSTTLTALAAANPALPSPDFKTIID 1132
Db 1138 KLTRHVTVPPLGSLRTAQTQSRKLPSTTLTALAAANPALPSPDFKTIID 1189

RESULT 37
US-10-877-022-613

Sequence 613, Application US/10877022
Publication No. US2004024763A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,022

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/05/432,503

FILING DATE: 02-Nov-1999

APPLICATION NUMBER: 08/974,549

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-May-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-Oct-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:

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REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 613:

SEQUENCE CHARACTERISTICS:

LENGTH: 1189 amino acids

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1189
OTHER INFORMATION: /note= "fusion protein composed of
melittin signal sequence and full length
hTERT protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-10-877-022-613

Query Match 99.8%; Score 5952; DB 17; Length 1189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVERLGPQWRVYQGDPAAFALVAQCLVCPM 60
Db MPAPRCRAVRSLLRSHYREVLPATFVERLGPQWRVYQGDPAAFALVAQCLVCPM 117
QY 61 DAPPPAPSPFQVSCLEKELVAEVLQRLCEBKAQNTLARGFALLDGRGPPPAFTTSR 120
Db DAPPPAPSPFQVSCLEKELVAEVLQRLCEBKAQNTLARGFALLDGRGPPPAFTTSR 177
QY 118 DAPPPAPSPFQVSCLEKELVAEVLQRLCEBKAQNTLARGFALLDGRGPPPAFTTSR 177
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Db SYLPTVTDLARSGAMGLLRRVGDVVLHLARCALFLVAPSCAYVCGPPLYQLGA 237
QY 181 ATQAPPPHAGSPRRRLGCBRAVNSVREAGVPLGLPAPGARSGASASRLPLPRPR 240
Db ATQAPPPHAGSPRRRLGCBRAVNSVREAGVPLGLPAPGARSGASASRLPLPRPR 297
QY 241 GAAPPEERTVGGGSAHQRTRGPDGFCVSPAPRAEATSLGALSGTRHSPVSG 300
Db GAAPPEERTVGGGSAHQRTRGPDGFCVSPAPRAEATSLGALSGTRHSPVSG 357
QY 298 GAAPPEERTVGGGSAHQRTRGPDGFCVSPAPRAEATSLGALSGTRHSPVSG 357
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Db ROHNAEPSTSRPPRPMWTPCPVVAETKHPLYSSGDKQLRPSLLSLRSTLGARRL 417
QY 358 ROHNAEPSTSRPPRPMWTPCPVVAETKHPLYSSGDKQLRPSLLSLRSTLGARRL 417
Db ROHNAEPSTSRPPRPMWTPCPVVAETKHPLYSSGDKQLRPSLLSLRSTLGARRL 477
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Db PAAGVAREKPGQSVAPAEEDTDPRRLVQLRQSSPQVGFYACILRLVPPGLMS 537
QY 478 PAAGVAREKPGQSVAPAEEDTDPRRLVQLRQSSPQVGFYACILRLVPPGLMS 537
Db PAAGVAREKPGQSVAPAEEDTDPRRLVQLRQSSPQVGFYACILRLVPPGLMS 597
QY 481 RHNERFLNTKFKFISLGKAKLSLOELTWKMSVSDCAMLRRSPGVCPAAEHLREBI 540
Db RHNERFLNTKFKFISLGKAKLSLOELTWKMSVSDCAMLRRSPGVCPAAEHLREBI 597
QY 538 RHNERFLNTKFKFISLGKAKLSLOELTWKMSVSDCAMLRRSPGVCPAAEHLREBI 597
Db RHNERFLNTKFKFISLGKAKLSLOELTWKMSVSDCAMLRRSPGVCPAAEHLREBI 657
QY 541 LAKEFLHMLSVYVELRSPFYVTEETTPQKSLFYPSPVMSKLSIGRQLKXVQJRE 600
Db LAKEFLHMLSVYVELRSPFYVTEETTPQKSLFYPSPVMSKLSIGRQLKXVQJRE 657
QY 598 LAKEFLHMLSVYVELRSPFYVTEETTPQKSLFYPSPVMSKLSIGRQLKXVQJRE 657
Db LAKEFLHMLSVYVELRSPFYVTEETTPQKSLFYPSPVMSKLSIGRQLKXVQJRE 717
QY 601 LSEAEVQRERAPALITSLRFLPKPDGLRPIVANDVYVAGARTRRERARLTSRYKA 660
Db LSEAEVQRERAPALITSLRFLPKPDGLRPIVANDVYVAGARTRRERARLTSRYKA 717
QY 658 LSEAEVQRERAPALITSLRFLPKPDGLRPIVANDVYVAGARTRRERARLTSRYKA 717
Db LSEAEVQRERAPALITSLRFLPKPDGLRPIVANDVYVAGARTRRERARLTSRYKA 777
QY 661 LSEAEVQRERAPALITSLRFLPKPDGLRPIVANDVYVAGARTRRERARLTSRYKA 777
Db LSEAEVQRERAPALITSLRFLPKPDGLRPIVANDVYVAGARTRRERARLTSRYKA 837
QY 721 PODRLTEVIAIIPKQNTYCVRRYAVVQKAAHGHVKAESKHSVTLTDLQPMRQFVAHL 780
Db PODRLTEVIAIIPKQNTYCVRRYAVVQKAAHGHVKAESKHSVTLTDLQPMRQFVAHL 837
QY 778 PODRLTEVIAIIPKQNTYCVRRYAVVQKAAHGHVKAESKHSVTLTDLQPMRQFVAHL 837
Db PODRLTEVIAIIPKQNTYCVRRYAVVQKAAHGHVKAESKHSVTLTDLQPMRQFVAHL 897
QY 781 QETSPLRDAVVEQSSSLNEASSGLFDVLRMCHAVIRKSKSVYVQCGLPQSSILSTL 840
Db QETSPLRDAVVEQSSSLNEASSGLFDVLRMCHAVIRKSKSVYVQCGLPQSSILSTL 897
QY 838 QETSPLRDAVVEQSSSLNEASSGLFDVLRMCHAVIRKSKSVYVQCGLPQSSILSTL 897
Db QETSPLRDAVVEQSSSLNEASSGLFDVLRMCHAVIRKSKSVYVQCGLPQSSILSTL 900
QY 841 LQSLCYGDMENKLFAGIRRDGLLRVDDFLVLTPEHLTHAKTFLTLVAGVEYGVVNL 900
Db LQSLCYGDMENKLFAGIRRDGLLRVDDFLVLTPEHLTHAKTFLTLVAGVEYGVVNL 900

Db 898 LCSLCYGDMEKLFAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVGVEYCVNL 957
QY 901 RKTIVNPFVDEALGTAFAVQMPAHGLFPWCGLLLDTRTLEVOSSVARTSTRASYTF 960
Db 958 RKTIVNPFVDEALGTAFAVQMPAHGLFPWCGLLLDTRTLEVOSSVARTSTRASYTF 1017
QY 961 NRGEKAGRNRRKLFVLRKCHSLFLDLQVNSLQVCTNIYKILLLOAYRFHACVLOLP 1020
Db 1018 NRGEKAGRNRRKLFVLRKCHSLFLDLQVNSLQVCTNIYKILLLOAYRFHACVLOLP 1077
QY 1021 FHQGWKNPFFLRVSDTSLCYSILKAKAGNSLGAAGAAGPLSEAVOWLCHQAFLL 1080
Db 1078 FHQGWKNPFFLRVSDTSLCYSILKAKAGNSLGAAGAAGPLSEAVOWLCHQAFLL 1137
QY 1081 KLFRHRTVYVLLGSLRTAQTOLSRKLPGLTLLALEAANPALPSPDKTLLD 1132
Db 1138 KLFRHRTVYVLLGSLRTAQTOLSRKLPGLTLLALEAANPALPSPDKTLLD 1189

RESULT 38
US-10-044-692-324
Sequence 324, Application US/10044692
Publication No. US20030096344A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SRO ID NO: 324:
SEQUENCE CHARACTERISTICS:

LENGTH: 1200 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 324:
US-10-044-692-324
Query Match 99.8%; Score 5952; DB 14; Length 1200;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPARACAVNSLSLSHREVPLATFVRRLGPGQMRVVGQDPAPAFALVAQCLVCVPM 60
Db 69 MPARACAVNSLSLSHREVPLATFVRRLGPGQMRVVGQDPAPAFALVAQCLVCVPM 128
QY 61 DARPPAPSPFQVSCLELVARVLQRLCERGAQVLAFCALDGAAGSPPEAFTTSVR 120
Db 123 DARPPAPSPFQVSCLELVARVLQRLCERGAQVLAFCALDGAAGSPPEAFTTSVR 188
QY 121 SYLPTVTDALRGSGAMGLLRVGDVYLVAHLARCALFVLA8CAVQVCGPPLVQCA 180
Db 189 SYLPTVTDALRGSGAMGLLRVGDVYLVAHLARCALFVLA8CAVQVCGPPLVQCA 248
QY 181 ATOARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRGGSASRSLPLKPRR 240
Db 249 ATOARPPHAGSPRRRLCERAMNHSVREAGVPLGLPAPGARRGGSASRSLPLKPRR 308
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Db 309 GAAPERPPTVQGSMAHPRGTRGSDRGFCVSPAPAEABATSLGALSCTRHSHPVG 368
QY 301 RQHHAGPSTSPRPWPMTPCPPVVAETKHFLLYS8GDEQRLPSTLSLSLPGARL 360
Db 369 RQHHAGPSTSPRPWPMTPCPPVVAETKHFLLYS8GDEQRLPSTLSLSLPGARL 428
QY 361 VETIFGSRPMPGPRRLPLRQRYWQMRPFLLELGNHACCPYGLLKTHCPRLAAVT 420
Db 423 VETIFGSRPMPGPRRLPLRQRYWQMRPFLLELGNHACCPYGLLKTHCPRLAAVT 488
QY 421 PAAGVCAAREKPOGSAPEEDTDPRRLVOLIRQSSWQYGFVACLRRLVPPGLMS 480
Db 489 PAAGVCAAREKPOGSAPEEDTDPRRLVOLIRQSSWQYGFVACLRRLVPPGLMS 548
QY 481 RHNERPRLNKKFISLGHAKLSLOELTWKMSVDCAMLRSPVGCVPAAEHRLREI 540
Db 549 RHNERPRLNKKFISLGHAKLSLOELTWKMSVDCAMLRSPVGCVPAAEHRLREI 608
QY 541 LAKFLHMLSVYVVELLSFFVETTFQKNELPFYRDSWSKLSIGIRQLKRVQURE 600
Db 609 LAKFLHMLSVYVVELLSFFVETTFQKNELPFYRDSWSKLSIGIRQLKRVQURE 668
QY 601 LSEAEVRQHRKRPALITSRLFIKPDGLRITVMDVVGARTRRKREARLSRYKA 660
Db 669 LSEAEVRQHRKRPALITSRLFIKPDGLRITVMDVVGARTRRKREARLSRYKA 728
QY 661 LFSVLYNERARRPGLLGASVGLDIDHRAWRTFVLRVAQDPPEPLFYKQDVDTGAYDTI 720
Db 729 LFSVLYNERARRPGLLGASVGLDIDHRAWRTFVLRVAQDPPEPLFYKQDVDTGAYDTI 788
QY 721 PODRLTEVYASIIKQONTYCVRRYAVQXAAHGRKAFKSVSTLTDLPQMRQFVAHL 780
Db 789 PODRLTEVYASIIKQONTYCVRRYAVQXAAHGRKAFKSVSTLTDLPQMRQFVAHL 848
QY 781 QETSPLRDAVVEQSSSLNEAS8GLFDVFLRMCHAVRIRKSVYQCGI8Q8ILSTL 840
Db 849 QETSPLRDAVVEQSSSLNEAS8GLFDVFLRMCHAVRIRKSVYQCGI8Q8ILSTL 908
QY 841 LCSLCYGDMEKLFAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVGVEYCVNL 900
Db 909 LCSLCYGDMEKLFAGIRRDGILLRLVDDFLVTPHLTHAKTFLRTLVGVEYCVNL 968
QY 901 RKTIVNPFVDEALGTAFAVQMPAHGLFPWCGLLLDTRTLEVOSSVARTSTRASYTF 960

Db 969 KRTVNFPEDEALGTAFAVQMPAHGLFPMWGLLDTRILEVQSDYSYARSISASLT 1028
 QY 961 NRGFKAGRMRRKLFVGLRKCHSLFLDLQVNSLQVCTNIIYKILLQAYRFHACVLQLP 1020
 Db 1029 NRGFKAGRMRRKLFVGLRKCHSLFLDLQVNSLQVCTNIIYKILLQAYRFHACVLQLP 1088
 QY 1021 FHQVWKNPTFFLRVSDTASLCYSILKKNAGMSGAGGAGPLPSEVWGLCHQATLL 1080
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 QY 1081 KLTRHRTVYVPLGLSLRTAQOTLSRKLPGTTLTALAAANPALPSDFKTIID 1132
 Db 1149 KLTRHRTVYVPLGLSLRTAQOTLSRKLPGTTLTALAAANPALPSDFKTIID 1200

RESULT 39
 US-10-044-539-324
 Sequence 324, Application US/10044539
 Publication No. US20030100093A1
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
 THERAPEUTIC METHODS
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/044,539
 FILING DATE: 11-Jan-2002
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/912,951
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-May-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-May-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-Apr-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-Oct-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 324:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1200 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear

MOLECULE TYPE: Protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 324:
 US-10-044-539-324

Query Match 99.8%; Score 5952; DB 14; Length 1200;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSILRSRYREVPLATFVRRLGQGGRRLVORGDPAPFALVAOCLVGVW 60
 Db 69 MPRAPRCRAVRSILRSRYREVPLATFVRRLGQGGRRLVORGDPAPFALVAOCLVGVW 128
 QY 61 DAPPAPAPSPFQVSCIKELVAVRLQRLCERGAQVLAEGFALLDARGGPREAFTTSR 120
 Db 129 DAPPAPAPSPFQVSCIKELVAVRLQRLCERGAQVLAEGFALLDARGGPREAFTTSR 188
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 Db 189 SYLNTVTDALRSGGAWGLILRRVGDVLYHLIARCALVLYVAPSCAYVCGPPLYQLCA 248
 QY 181 ATQARPPHASPGRRLGGERANHSVREAGVPLGPAFGARRGGASASRLPLPRPRR 240
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 QY 301 RQHHAGPSTSRPRRWDPCPPVYAEYHFLYSSGDKQLPSFLSLSRSLTARPL 360
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 QY 361 VETIFLGSRPWPGTFRRLPLRQRYWQMRPLFLELIGNHAOCPYGVLLKTRCPJRAAVT 420
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 QY 481 RHNERFRLNTKFFISLGHAKLSLOELTWKMSVRCAMLRSPGVCPAAEHRLREI 540
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 Db 609 LAKFLHMSVYVELLRSPFYVTEFTFQKNRLFYRPSVMSKLOSIGIRQLKRVQLRE 668
 QY 601 LSAEVRQHRBARPALTLRLRFLPKDGLRPIVMNDVYVGARTRRERARLRSRYKA 660
 Db 669 LSAEVRQHRBARPALTLRLRFLPKDGLRPIVMNDVYVGARTRRERARLRSRYKA 728
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 Db 729 LPSVLNYERARRRGLGASVLDLIDIRAMRTFVLRAQDPPPELYFYKVDVTGAYDTI 788
 QY 721 PQURLFEVLAIIKPNQTCVRRYAVVQAAAGHGRKAFKSNVSLTDLQPMRGFVALH 780
 Db 789 PQURLFEVLAIIKPNQTCVRRYAVVQAAAGHGRKAFKSNVSLTDLQPMRGFVALH 848
 QY 781 QETSPLDAVVIQSSSLNEASGLFDVLRFMCHAAVIRKSYVVOCGIIPQGSILSL 840
 Db 849 QETSPLDAVVIQSSSLNEASGLFDVLRFMCHAAVIRKSYVVOCGIIPQGSILSL 908
 QY 841 LGLCYGMENKLPAGIRPDGLILRLVDDPLLVTPLTHAKTFLTLVGVGEYGVNLL 900
 Db 909 LGLCYGMENKLPAGIRPDGLILRLVDDPLLVTPLTHAKTFLTLVGVGEYGVNLL 968
 QY 901 KRTVNFPEDEALGTAFAVQMPAHGLFPMWGLLDTRILEVQSDYSYARSISASLT 960
 Db 969 KRTVNFPEDEALGTAFAVQMPAHGLFPMWGLLDTRILEVQSDYSYARSISASLT 1028
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Db 1029 NRGKAGNNRRKLFVYLRLKCHSLFDLQVNSIQVCTINIYKLLIQARFPAQVQLP 1088
 Qy 1021 FHQGVKNPFFLEVIDSLASLCSILKAKNAGSLGAKGAGPLPSEAVQWLCQAFL 1080
 Db 1089 FHQGVKNPFFLEVIDSLASLCSILKAKNAGSLGAKGAGPLPSEAVQWLCQAFL 1148
 Qy 1081 KLTFRRTYVPLGLSLTAQOTLSRKLPGLTLTLEAANPALPSDKTLLD 1132
 Db 1149 KLTFRRTYVPLGLSLTAQOTLSRKLPGLTLTLEAANPALPSDKTLLD 1200

RESULT 40

US-10-325-810-612

Sequence 612, Application US/10325810

Publication No. US20030204069A1

GENERAL INFORMATION:

APPLICANT:

Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESSES:

ADDRESSER: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181

FILING DATE: 29-Sep-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-Oct-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-May-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausehus, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 612:

SEQUENCE CHARACTERISTICS:

LENGTH: 1200 amino acids

TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1200
 OTHER INFORMATION: /note="fusion protein composed of His6
 and Anti-Xpress tags", enterokinase
 cleavage site and full length hTert
 protein"
 SEQUENCE DESCRIPTION: SEQ ID NO: 612:
 US-10-325-810-612

Query Match 99.8%; Score 5952; DB 14; Length 1200;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRLSLRSHREVLPATFVRRLGPOGMRVORQDPAPAPALVAQCLVCPM 60
 Db 69 MPAPRCRAVRLSLRSHREVLPATFVRRLGPOGMRVORQDPAPAPALVAQCLVCPM 128
 Qy 61 DARPPAAPSFRQVSLKELVAVYQLRCEGAKNVLAFGALLDGAAGPEAFTSVR 120
 Db 129 DARPPAAPSFRQVSLKELVAVYQLRCEGAKNVLAFGALLDGAAGPEAFTSVR 188
 Qy 121 SYLPTVTDALRGSGAMGLLRVGDVYLHLARCALFVLVAPSCAYQVGPPIYOLGA 180
 Db 189 SYLPTVTDALRGSGAMGLLRVGDVYLHLARCALFVLVAPSCAYQVGPPIYOLGA 248
 Qy 181 ATQARPPIHAGSPRRRLGCERAMNHSVREAGVPLGLPAPGARRRGASRSILPEKPRR 240
 Db 249 ATQARPPIHAGSPRRRLGCERAMNHSVREAGVPLGLPAPGARRRGASRSILPEKPRR 308
 Qy 241 GAAPPERTPVQGGSMANPGRTRGSDRGFCVVSAPAPAEATSLFEGALSGTRHSHSVG 300
 Db 309 GAAPPERTPVQGGSMANPGRTRGSDRGFCVVSAPAPAEATSLFEGALSGTRHSHSVG 368
 Qy 301 ROHHAQPPSTSRPPMDTPCPVYAEFKHFLYSSGDEQLRPSFLSLSPSLTGARRL 360
 Db 369 ROHHAQPPSTSRPPMDTPCPVYAEFKHFLYSSGDEQLRPSFLSLSPSLTGARRL 428
 Qy 361 VETITLGRPPMGTPTPRRLPLPORYWQMRPLFLELNNHAQCPYVILLKTHCPRAAVT 420
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 Db 489 PAAGVCAREKPGQSVAAPEEDTDPRLVOLLROHSSWQYGFYACLRLLVPPGLMGS 548
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 Db 549 RNNRRPRLNTKFFSLGKHAKLSTQELTWKNSVYDCAMLRSPQVGCVPAAHRLREI 608
 Qy 541 LAKELHMLMSYVYVGLLSPFYVETTFQKRLPFYRSVWSKQSIIRHKLKRVQRE 600
 Db 609 LAKELHMLMSYVYVGLLSPFYVETTFQKRLPFYRSVWSKQSIIRHKLKRVQRE 668
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 Db 669 LSEAEVRQHRARPALTLTSLRFLPKPDGLRPIVMDVVGARFRRRKRERLTSRYKA 728
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 Db 729 LFSVNTYRRARPGLLGASVGLDIDIRAWRTFVLRYAQPPELRYVKVDYGAAYTI 788
 Qy 721 PODRLTEVIASIKPQNTYCVRYAVVOKAAHGHRKAFKSHVSTLTLQPYMGQFVAHL 780
 Db 789 PODRLTEVIASIKPQNTYCVRYAVVOKAAHGHRKAFKSHVSTLTLQPYMGQFVAHL 848
 Qy 791 QETSLPRLAVVIEQSSSLNEASSGLFDVFLRPMCHHVRIRGKSYVQCGIIPQGISLTL 840
 Db 849 QETSLPRLAVVIEQSSSLNEASSGLFDVFLRPMCHHVRIRGKSYVQCGIIPQGISLTL 908

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QY 841 LCSLCYGMENKLFAGIRRDGILLRLVDDPELLVTBPLTHAKTELRTLVGVPEYGVYNI 900
Db 909 LCSLCYGMENKLFAGIRRDGILLRLVDDPELLVTBPLTHAKTELRTLVGVPEYGVYNI 968
QY 901 RKTIVNFPVEDEALGGTAFCMPAHGLFPMCGLLDTRTLEVQSDYSSYARTSIRASYTF 960
Db 969 RKTIVNFPVEDEALGGTAFCMPAHGLFPMCGLLDTRTLEVQSDYSSYARTSIRASLTF 1028
QY 961 NRGFKAGRMRRKTLFVLRKCHSLFLDQVNSLQTVCTNIYKILLLOAYRFHACVLQLP 1020
Db 1029 NRGFKAGRMRRKTLFVLRKCHSLFLDQVNSLQTVCTNIYKILLLOAYRFHACVLQLP 1088
QY 1021 FHOQVKNPTFPLRVISDPTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1089 FHOQVKNPTFPLRVISDPTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1148
QY 1081 KLTRHRVTYVPLIGSLRTAQOTLSRKLPGTTLTALBAANPALPSDFKTIID 1132
Db 1149 KLTRHRVTYVPLIGSLRTAQOTLSRKLPGTTLTALBAANPALPSDFKTIID 1200

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 Job time : 188 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2004, 15:50:35 ; Search time 26 Seconds

(without alignments)
4189,130 Million cell updates/sec

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Perfect score: 5963
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 120 summaries

Database :
1: PIR.79: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5952	99.8	1132	2	T03844
2	717.5	12.0	1123	2	T51517
3	588.5	9.9	989	2	T03838
4	388	6.5	1132	2	T31107
5	357	6.0	1117	2	T14891
6	355.5	6.0	884	2	S53396
7	175.5	2.9	3530	2	A59266
8	172.5	2.9	660	1	Q08E3
9	142.5	2.4	1560	1	T00080
10	140.5	2.4	1892	1	T18314
11	140	2.3	1460	1	EDBE1F
12	139.5	2.3	3511	2	A59295
13	139.5	2.3	552	2	F75311
14	138.5	2.3	924	2	S27923
15	135	2.3	1356	1	C45219
16	134	2.2	606	1	G75302
17	133	2.2	1106	2	J000405
18	132.5	2.2	946	2	J007810
19	131.5	2.2	1184	2	G01763
20	131	2.2	916	2	JT00396
21	131	2.2	1446	1	A4534
22	130.5	2.2	1184	2	S50832
23	130.5	2.2	2715	2	T13049
24	130	2.2	1067	2	T18156
25	129.5	2.2	383	2	S32975
26	129	2.2	403	2	S52796
27	129	2.2	403	2	S55543
28	128.5	2.2	628	2	S01955
29	128	2.1	376	2	C75580

30	128	2.1	1776	2	G86280	protein T5E21.13 (
31	127.5	2.1	1048	2	T31425	C-terminal domain-
32	127	2.1	260	2	S22373	proline-rich prote
33	127	2.1	505	2	S72273	actin-depolymerizi
34	127	2.1	580	2	T43481	probable mucin DKF
35	127	2.1	847	1	A53800	mixed-lineage proc
36	127	2.1	862	2	T46289	hypothetical prote
37	127	2.1	1039	2	T35878	hypothetical prote
38	126.5	2.1	603	2	H75272	probable nucleic a
39	126	2.1	330	2	B98119	transposase, uncha
40	125.5	2.1	574	2	T43556	Wiskott-Aldrich sy
41	125.5	2.1	574	2	T38819	viral proteinase -
42	125	2.1	522	2	S52216	tenascin Y precurs
43	125	2.1	1914	2	T42635	N-methyl-D-asparta
44	124	2.1	1298	1	EDBE75	hypothetical prote
45	124	2.1	1323	2	S27224	hypothetical prote
46	123.5	2.1	381	2	S16506	synapsin Ia - rat
47	123.5	2.1	704	2	A30411	68.6k capsid prote
48	123	2.1	646	1	WZBEC8	salivary proline-r
49	122.5	2.1	310	1	PIHUSD	hypothetical prote
50	122.5	2.1	635	2	F75477	hypothetical prote
51	122.5	2.1	915	2	T12526	otogelin - mouse
52	122.5	2.1	2910	2	T42214	MHC class III hist
53	122	2.0	1870	2	S37671	hydroxyproline-ric
54	121.5	2.0	620	2	S06733	guanylate cyclase
55	121.5	2.0	1102	2	UH0717	period protein PBR
56	121.5	2.0	1257	2	T13957	MHC class III hist
57	121	2.0	2142	2	B35098	lipoxygenase (EC 3.
58	120.5	2.0	335	2	T05722	probable proline-r
59	120.5	2.0	891	2	G84693	ataxin-2 - mouse
60	120.5	2.0	1285	2	T14171	probable membrane
61	120	2.0	509	2	T34871	BOLE1 protein - hu
62	120	2.0	1239	1	Q0E810	DNA-directed RNA p
63	120	2.0	1859	1	A34092	DNA-directed RNA p
64	120	2.0	1862	2	T29959	MHC class III hist
65	120	2.0	1872	2	S36152	hypothetical prote
66	120	2.0	2793	2	B90784	hypothetical prote
67	120	2.0	2806	2	D85644	hypothetical prote
68	119.5	2.0	361	2	T12543	hypothetical prote
69	119.5	2.0	775	1	EDBE11	immediate-early pr
70	119	2.0	639	2	G02919	transcription fact
71	119	2.0	7576	2	T17428	FK506 polyketide s
72	118.5	2.0	628	2	S19150	hypothetical prote
73	118.5	2.0	751	2	D98320	hypothetical prote
74	118.5	2.0	903	2	T00705	N-chimerin homolog
75	118.5	2.0	1334	2	T50568	probable multi-dom
76	118.5	2.0	2796	2	UC4743	fatty-acid synthas
77	118.5	2.0	3164	1	WMBEH6	Uls6 protein - hum
78	118	2.0	548	2	S52735	CW17R protein - mo
79	118	2.0	2352	2	C83229	probable non-ribos
80	117.5	2.0	312	2	A51129	hypothetical prote
81	117.5	2.0	576	2	T36729	probable serine/th
82	117.5	2.0	1222	2	T22490	hypothetical prote
83	117.5	2.0	2944	2	A54849	collagen alpha 1(V
84	117	2.0	300	2	S19560	proline-rich prote
85	117	2.0	512	2	B54337	F02569.2 protein l
86	117	2.0	684	2	T36771	probable integral
87	117	2.0	691	2	A25704	synapsin I - rat
88	117	2.0	1467	2	T18411	larophillin-1, bra
89	117	2.0	1472	2	T18413	larophillin-1, bra
90	116.5	2.0	434	1	WMBE73	Uls3 protein - hum
91	116.5	2.0	1174	2	B85740	probable oxidoredu
92	116.5	2.0	1174	2	H90878	hairless protein -
93	115.5	1.9	1182	2	T48378	hypothetical prote
94	115.5	1.9	1322	2	T23140	proline-rich prote
95	115	1.9	301	2	E29149	proline-rich prote
96	115	1.9	309	2	S10889	50kD proline rich
97	115	1.9	456	2	T35474	membrane transloc
98	115	1.9	629	2	E47096	probable DNA-bind
99	115	1.9	753	2	G87178	DNA-binding protei
100	115	1.9	767	2	S41479	protein-tyrosine k
101	115	1.9	1091	2	S33596	DNA-binding protei
102	115	1.9	2282	2	T42717	

103 114.5 1.9 256 2 A60533 tumor-associated a
104 114.5 1.9 496 2 S26402 homeotic protein H
105 114.5 1.9 706 2 E30411 syntenic Ia - bovi
106 114.5 1.9 1069 2 S27922 nuclear antigen EB
107 114.5 1.9 1174 2 E64888 probable pyruvate
108 114.5 1.9 1541 2 T02831 AAA protein L4171.
109 114.5 1.9 1541 2 T35966 hypothetical prote
110 114.5 1.9 990 2 T14756 hypothetical prote
111 114.5 1.9 1696 2 T00057 hypothetical prote
112 113.5 1.9 295 2 B48013 proline-rich prote
113 113.5 1.9 649 2 A35816 transcription regu
114 113.5 1.9 1001 2 T50914 hypothetical membr
115 113.5 1.9 1085 2 T03531 cobb protein homol
116 113.5 1.9 1400 2 T31555 hypothetical prote
117 113.5 1.9 2176 2 T13806 human gene protei
118 113 1.9 543 1 UC4070 protein kinase (EC
119 113 1.9 1323 1 T78557 N-methyl-D-asparta
120 112.5 1.9 699 2 C43674 US4 protein - huma

ALIGNMENTS

RESULT 1
T03844
telomerase catalytic chain - human
N:Alternate names: telomerase reverse transcriptase
C:Species: Homo sapiens (man)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #ext_change 09-Jul-2004
C:Accession: T03844
R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.
S:Science 277, 955-959, 1997
A:Title: Telomerase catalytic subunit homologs from fission yeast and human.
A:Reference number: 215111, PMID:97400623, PMID:9252327
A:Accession: T03844
A:Status: Preliminary, translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1132 <NA>
A:Cross-references: UNIPROT:O14746; EMBL:AF015950; NID:G2330016; PIDN:AAC51672.1; PID:92
A:Experimental source: Kidney
C:Genetics:
A:Gene: TERT
A:Map position: 5p

Query Match 99.8%; Score 5952; DB 2; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSILRSYREVLPLATFVRRLGPQGRVLRGDPAPAFALVAQCCLVCPW 60
DB 1 MPAPRCRAVRSILRSYREVLPLATFVRRLGPQGRVLRGDPAPAFALVAQCCLVCPW 60

QY 61 DAPPPAASPRVSCLELVARVLOLCERGAKNVLAFFGALDAGSGPEAFTTSVR 120
DB 61 DAPPPAASPRVSCLELVARVLOLCERGAKNVLAFFGALDAGSGPEAFTTSVR 120

QY 121 SYLVNTVTDALRSGAGWGLLRVGVDDVLAHLLARCAFLVLAQSCAYQCCPPLVQGA 180
DB 121 SYLVNTVTDALRSGAGWGLLRVGVDDVLAHLLARCAFLVLAQSCAYQCCPPLVQGA 180

QY 181 ATGAPRPPHAGSGRRRLGGERAMNSVREAGVPLGIPAPGARRGSGASRSRLPLKRRR 240
DB 181 ATGAPRPPHAGSGRRRLGGERAMNSVREAGVPLGIPAPGARRGSGASRSRLPLKRRR 240

QY 241 GAAPFERTPVGGGVAHFGRTGSDRGFCVVSFAPPAEATSLGALSGTRHSPSVG 300
DB 241 GAAPFERTPVGGGVAHFGRTGSDRGFCVVSFAPPAEATSLGALSGTRHSPSVG 300

QY 301 RQHNAPRSTSRPRRWDTPCPVVAETGHLVSSGDEQLRPSLISLRSLGARLL 360
DB 301 RQHNAPRSTSRPRRWDTPCPVVAETGHLVSSGDEQLRPSLISLRSLGARLL 360

QY 361 VETIFGSRPMWGTFRRLPLRQRYQWRPLFLELIGNAACPPYGLTKTHCPRAAVT 420

DB 361 VETIFGSRPMWGTFRRLPLRQRYQWRPLFLELIGNAACPPYGLTKTHCPRAAVT 420

QY 421 PAAGVCAERKQDSVAAPBEEDTDPRLVOLLROHSSPMQVGFVACLRVLPPGLMGS 480
DB 421 PAAGVCAERKQDSVAAPBEEDTDPRLVOLLROHSSPMQVGFVACLRVLPPGLMGS 480

QY 481 RHNERRLNTKTFISIGKIAKLSLOELTWKMSVRCAMLRSPGVGCVPAAHRLREEL 540
DB 481 RHNERRLNTKTFISIGKIAKLSLOELTWKMSVRCAMLRSPGVGCVPAAHRLREEL 540

QY 541 LAKELHLMGVVVELLSFFVYETTFQKNRLFFPRSPWSKLQSIGIRHILKRYOLRE 600
DB 541 LAKELHLMGVVVELLSFFVYETTFQKNRLFFPRSPWSKLQSIGIRHILKRYOLRE 600

QY 601 LSEAEVQHEAPRALITSLRLTIPKPDGLPIVNDVYVGANTFRERAEHLTERVKA 660
DB 601 LSEAEVQHEAPRALITSLRLTIPKPDGLPIVNDVYVGANTFRERAEHLTERVKA 660

QY 661 LFSVLANERARPPGLIGASVLSGLDILHRAARTFVLRADQPPPELYFVKVDYTGAYDTI 720
DB 661 LFSVLANERARPPGLIGASVLSGLDILHRAARTFVLRADQPPPELYFVKVDYTGAYDTI 720

QY 721 PODELFEVIAIIRKQNTYCVRRYAVVQKAHGVKAPKSHVSTLTDLPYMRQFVAHL 780
DB 721 PODELFEVIAIIRKQNTYCVRRYAVVQKAHGVKAPKSHVSTLTDLPYMRQFVAHL 780

QY 781 QENSPLDVAIVIOSSSLNASSGLFDVLRFRCHAVLRGSAVQCCGIPGSLISLTL 840
DB 781 QENSPLDVAIVIOSSSLNASSGLFDVLRFRCHAVLRGSAVQCCGIPGSLISLTL 840

QY 841 LCSIQYDMDENKLFAGIRRDGLRLRVDELFLVPLHAKFLRLTVRGVEPGCVNL 900
DB 841 LCSIQYDMDENKLFAGIRRDGLRLRVDELFLVPLHAKFLRLTVRGVEPGCVNL 900

QY 901 RKYVNFPPVDEALGTAAPVQPAHGLFPVCGLLDTRLELVQSDVSSAFKSIKSLTF 960
DB 901 RKYVNFPPVDEALGTAAPVQPAHGLFPVCGLLDTRLELVQSDVSSAFKSIKSLTF 960

QY 961 NRGFKAGNRKRLFGVLRKCHSLFLDLQVNSLQVCTNITYKILLQVRFHACVQLP 1020
DB 961 NRGFKAGNRKRLFGVLRKCHSLFLDLQVNSLQVCTNITYKILLQVRFHACVQLP 1020

QY 1021 FHOQWKNPFFLRVISTDASISLILKAKNAGMSIGAKGAGLPSEAVQMLCHQAFLL 1080
DB 1021 FHOQWKNPFFLRVISTDASISLILKAKNAGMSIGAKGAGLPSEAVQMLCHQAFLL 1080

QY 1081 KLRHRVTVPLLSLRTAQTLSRKLPGTTLTALBAANPALPSDFKTIID 1132
DB 1081 KLRHRVTVPLLSLRTAQTLSRKLPGTTLTALBAANPALPSDFKTIID 1132

RESULT 2

T51517
telomerase reverse transcriptase - Arabidopsis thaliana
N:Alternate names: protein F5E19_190
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #ext_change 09-Jul-2004
C:Accession: T51517
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25394
A:Accession: T51517
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1123 <SAT>
A:Cross-references: UNIPROT:Q9SPU7; EMBL:AL391147
A:Experimental source: cultivar Columbia; BAC clone F5E19
C:Genetics:
A:Map position: 5
A:Introns: 100/3; 125/3; 147/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033/2
A>Note: F5E19_190

Query Match 12.0%; Score 717.5; DB 2; Length 1123;
 Best Local Similarity 23.7%; Pred. No. 9e-41;
 Matches 293; Conservative 199; Mismatches 512; Indels 233; Gaps 39;

1 MPRAFRCAVRSLRSHRYEVLPLATFV-----RRIGPOGWR-----L 38
 1 MPKRRKRVPEILRLFGNARNLNDALVDLIPRNIGPQCRGCGCCGSSDPAFL 60
 39 VQGRDPAFPAALVAQCLVCPMDAPPPAASFRQVSCLELVAVLQRL---CEGAKX 95
 61 LRSDPFIHYKRLIHRCFV-VLHEQTPDLDPSPFMSWQREIVERITIMQSGCD--CQX 117
 96 VLAFGFALLDGAAGPEAFTTSRSYLPNTVTDALRGSGAMGLLRVGDVVLILAR 155
 118 VICARYKYVOS-----SPILBLT-SSSWEFLLKRVGHDMVYLLQ 159

156 CALFVLVAPCAVQVCGPPYVQGAAT-----QARPPHASPGRRLGGERAMNSVRE 209
 160 TSIFLPLGKKHQVSGPPLCIKHKRTLSVENKRRKDDVQPTKQWLSAIVDCPKD 219
 210 AGVPLGLPAG-----ARRGGSASRLPLKRPKRA-----APEPRTVGGGSA 257
 220 DSATI-TPIVEGDVQHRKKTTRSRITLKRRKQKRVKFKVDCAPICTP----- 271
 258 HPGRTGRPSDRGFCVSPAPPAEATSLGALSGTRASHSPVGRQHHAGPSTSRPPRW 317
 272 ---STNGKVGSTG-----NDENMLHIGINGSLDFPVKAKQ----- 303

318 DTPCPVPAATKHELYS-SCDKQOLRPSFLLSLPSLIGARLVETITFGSPMMPGTP 376
 304 ---VKENKMKFGLSETYSVIPNHLIKTLRPQCSKLLMHIFEVVWMTSTPS 356
 377 RRLPLPQ-----RYMOKRPLFLELGNHACQPVGLKTCPC-----LRAAVPAG 424

357 HGKNCNGSSICLYHSLKSLKILGKTSSHLKMLDKPCVLLLOEDALKGTSSQS 416
 425 VCAREK---POGSVAA---PEEEDTPRLVQLRQHSMPQVYGFVACLRVLPPG 476
 417 --BRCKADKLPHGSSSQGTGPKCPVSEERKL-----YCTNQVVSFIWALCRYIVPS 468

477 LMSRHRERFLNRTKFTSLGKAKLSLOELTWKMSVRCAMLRSPGVCYPAEHL 536
 469 LIGTHOMRLVKRIAMFVSRRRNEKCTVQPLHKXSPFPFARKE--LCCWVNGHEL 526

537 REE-----ILAKFLHMSVYVLELSPFYVETTFQKRLFFPYRPSVSKLSIG 588
 527 QSESIRSTQMLCTKMWISWLFLEIVKLVHFNFYATESQGRINLIYYRRMSERLISKE 586

589 IROHLKRVQRELSAEVNRQHREARPALITSRLRFTPKDGLRPIYNDYVVGARFPERE 648
 587 ISALDQYVLDVAEASERRK-----LSKRFELPKANGVMVD-----FSSS 630

649 KRAERLTSRKALFSVINYERARRPGLLGASVGLDIDHMAWTFVLRYADQPP-PELY 707
 631 SRQGS-----RDTHAVIKDQIKKEPVLGSSVFDHDDFYNLCPYLILHRSQGEPLPY 686

708 FVKAVDTGAYDTIPQDRLEVIASIKPONTYCVRAVAVQKAGHG-----VRRAFKS 761
 687 FVAVADVFAKDSVDQKLLHVIOSFLKDE--YILNRCRLVCCGRSMWVKILVSSDKKS 744

762 HVTETLDQRYMGQFVANHLOETSPLRDAVYIEQSSINEMASGLFDVFLRFMHAVRIR 821
 745 NBRFRTSTVYNA-----LO-----STVVDKGENRVRKCDLMMVIGMLKNNMLQLD 792

822 GKSYVQCGIPQGISLSTLCSLCYGDMEKTLFAGI-----RRDGL----- 862
 793 KSFYVQIAGIPQGRILASLLCCFYGHLERTLILYFLLEASKOVSSKEGSEBELLIPTS 852

863 --LILRVDDDLVTLPHLTHAKTFLTLVRGVPEYGVYVNRKTYVNFVYDE----- 912
 853 YKLRFITDDVLFVSTSDQASSFYHRLKHGFKYCNKMNETKCFINFEDEEERCSGNR 912

913 --ALGTAFYQMPAHGLFPWCGLLDTRTLLEVQSDYSSYARTIRASVTEINRGFKAGRN 970

Db 913 FVGDNGVDFVR-----WTGLLINSRTFEQVDYTYTSLGHISSTSVAMQNPVNL 964

Qy 971 RRLFGVRLKCHS-FLDLQVNSLOTVCNTIYKILLQAYEFHACVLDLPFHQVWK-NP 1029
 965 ROKLCYFLVPKCHPLTFPSNINSSEIVANLIIQIFLLAMKHFHCYVEV---SRFKLHP 1021

Qy 1030 TFFLRVIDTSLSCYSIIKAKNAGSLGAK-GAAGPLPSEAVQVIMCHOAFLIKLTPHRTV 1088
 1022 CTFEFKITIVRYMYRLNRRVRRINTGSSFRPVKLKYEVEVIMGLDAYIQVLKKNSR 1081

Qy 1089 YVPLGLSLRTAQTO--LSRKLPGTTLTLEAANDAL 1123
 1082 YMLLIYKSLSKSLSLQQLSSSELRVATDRSNSSL 1118

Db 1082 YMLLIYKSLSKSLSLQQLSSSELRVATDRSNSSL 1118

RESULT 3
 telomerase catalytic chain - fission yeast (Schizosaccharomyces pombe)
 N.Alternate names: telomerase reverse transcriptase 1
 C.Species: Schizosaccharomyces pombe
 C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C.Accession: T03838; T03839; T40085
 R.Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.;
 Science 277, 955-959, 1997
 A.Title: Telomerase catalytic subunit homologs from fission yeast and human.
 A.Reference number: Z1511; MUID:97400623; PMID:9252327
 A.Accession: T03838
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-989 <NAK>
 A.Cross-references: UNIPROT:013339; EMBL:AF015783; NID:92340167; PIDN:AAC49803.1; PID:92:
 A.Experimental source: strain 972h(-)
 A.Accession: T03839
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-524,526-989 <LYN>
 A.Cross-references: EMBL:AF015783; NID:92340167; PIDN:AAC49802.1; PID:g2340168
 R.Lynn, M.; Raftery, M.A.; Barrett, B.G.; Volckaert, G.
 submitted to the EMBL Data Library, March 1998
 A.Reference number: Z21904
 A.Accession: T40085
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-524,526-989 <LYN>
 A.Cross-references: EMBL:AF015783; NID:92340167; PIDN:AAC49802.1; PID:g2340168
 A.Experimental source: strain 972h-, cosmid c29A3
 C.Genetics:
 A.gene: trt1, SPBC29A3.14c
 A.Map position: 2
 A.Introns: 86/3; 113/3; 153/2; 241/1; 372/1; 395/3; 485/3; 524/3; 582/2; 644/1; 693/3; 76
 C.Keywords: alternative splicing

Query Match 9.9%; Score 588.5; DB 2; Length 989;
 Best Local Similarity 22.2%; Pred. No. 4.9e-32;
 Matches 237; Conservative 202; Mismatches 381; Indels 247; Gaps 42;

5 PCRAVRSLRSHRYEVLPLATFVRLQPGQMRVLQVQSDPAFPAALVAQCT----- 55
 7 PKSRILR-FLNQVYYLTLINDYV-----QLVLRGSSPASYSNICEIRLSVDYQTSFS 57

Qy 56 -----VCPMDARPPPAASFRQVSCLELVAVLQRL---LQ----- 116
 58 IFLHSTVVGFDSPKDEGV-QFSPPKQSSSELIANVVKQMFESFERRRNLMLKGFSMNHE 116

Qy 106 GARGPPPAFTTSVASYLPNTVTDALRGSGAMGLLRVGDVVLHLLARCALFVLVAPS 165
 117 DFRAMHVGQNDLVSTFPNVLISILE-SKNWQMLLEIGSDAMHYLLSKSISIFALND 175

Qy 166 CAYQVCGPPLVQLGAAIATGAPPPHASPGRRLGGERAMNSVREAGVPLGLPAGARRG 225
 176 NYLQISGIPLRF-----NNVFEEYV-----SKRRK 200


```

QY 226 GSASRLPLPRRGAABERTPVGQSMHGPRTGRPSDGFVSPARPAEATSL 285
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 201 RTIETSIQNKARK-----EWSM----- 219
QY 286 EGALSTGRHS--HPSVGRQHNAQPPSTSPRPMDTPCPVYAEFKR-LYSSGKEDLR 342
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 220 -NSISISRSISFIYRSYKK-----FKQDLYNLHSICRNTVH 256
QY 343 PSLTSLSLPSTLTG-----ARRIVETIPLGSRPMWGPTRRL-----RLRPQWQMBPL 392
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 --MLQWIFPRQGLINAFQVQKHKVPLVQSQIV--VPKRLKLVPIELQTAQLRI 312
QY 393 FELLGNHAQCPYGVLLKTHCPRAAVTPPAGVCAREKQGSVAPEEDTPRLVOLL 452
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 313 SLKSVYNH-YCPY--IDTH-----DE-----XIL 334
QY 453 RQHSPPWQYGFPACTRLVPPGLWGSRHNERRLRNTKRLSLGKNAKLSLOELTKM 512
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 335 SYSLAKNQVAFRSLIVLVPFKLIMGNQRIETILKDLLETFLKLSRESFSLHLYMNI 394
QY 513 SVRDCAML--RSPGVCVPAEHRRLREELAKFLHMLMSVYVVELLRSEFYVTEFTQ 569
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 395 KISEIMVLVIGKRSNAKML--SDEPKRQIPAEFIYMLYNSFILIPILQSFYITESDL 452
QY 570 KRLFPYRPSWSKLSIGIRQLKRVQURELSEAEVQRHARALTSRLRFTPKRDG 629
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 453 RRTYVFRKDIW-KLCRPFITSMKAEKINENNVNDTQ-KTLLPDAVIRLIPKXNT 510
QY 630 LRPVMDVYVGARTFREREKRAERLTSRYKALFVLYNEBARP-----GLLGASVGL 683
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 511 FRITNL-----RKRFLIKQMSNMKMLVST--NQLTRPVASILKHLINNESSGI 558
QY 684 D--DIHRMRTF--VLEVRADPPPELYFVKVDVTGAYDTIPDDRLEVIASITKQN 737
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 559 PEMLEVYMKLLTFPKDILGHRWFG--RKCYFVRIDIKSCYDRIKODLMFRYKKLKQPE 616
QY 738 TYCVREYAAVQAAGHVAKFAKSHVSTLTDLPVNRQVVAHLOETSPLRDAVTEGSS 797
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 617 -FVIRKXATIH-ATSRRAKRVSEAFSFDVNPPEKVVQLSKMTS---DLTPDEPDY 671
QY 798 LNEASSGLFDVLFEMCHAVIRKGSYVQCGIPQGSILSTLLCSLCYGMENKLPAGI 857
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 672 WTKSSSEIFPMLEKHEHLSGIVKINSQYLOKVGIPQGSILSTLLCFWEMEDLIDELFT 731
QY 858 RRRG-LLRVLDDELIVPHLTHAKTFLTLVRGPEYCVVNAKTVNPFVEDEALG 916
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 732 KKKGSVLLRVVDPLFTVKKDAKFFLNLGRGFKHNFSTLSEKTVINENSGIINN 791
QY 917 TAFVQMPAHGLFPWCGILDTFTLEY-----QSDYSYARTSIRASVTFNRFKXGRNR 971
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 792 TEFNESEKR--WPFPGFSVNMRSUDTLACPKIDEALFNSISTVELTKMGKSF----- 842
QY 972 RKLFGVLRKCHS--LFLDLOVNSIQVCTNIYKI-----LLDAY 1010
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 843 --FYKILRSSLASPAQVFDITHNSKFNSCNIYRIGYSMCRQAY 887

RESULT 4
Telomerase reverse transcriptase - Oxytricha trifallax
C/Species: Oxytricha trifallax
C/Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C/Accession: T31107
R: Bryan, T.M.; Speger, J.M.; Chapman, K.B.; Cech, T.R.
Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998
A/Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and Oxytricha
A/Reference number: Z20985; PMID:98337940; PMID:9671703
A/Accession: T31107
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1132 <BRY>
A/Cross-references: UNIPROT:O76332; EMBL:AF060230; NID:93342795; PID:93342796; PIDN:AA03
C/Genetics:

```

```

A/Gene: TERT
Query Match 6.5%; Score 388; DB 2; Length 1132;
Best Local Similarity 22.1%; Pred. No. 3e-18;
Matches 136; Conservative 117; Mismatches 299; Indels 64; Gaps 17;

QY 450 QLRQHSPPWQYGFPACTRLVPPGLWGSRHNERRLRNTKRLSLGKNAKLSLOELT 509
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 451 QLFYQDQDQQLISNLFTEFVAFNFPKPFLEGR-NKKIFNMKMLQFVKFRFSFTKISLL 509
QY 510 WKXSVDCAMLRSPGVCVPAEHR--RLREELAKFLHMLMSVYVVELLRSEFYVTEFT 566
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 510 NKFRVNSWL-----SPKCDENKKEFMNENHVPFKVLKMPFEDALITLMRCYFSTK 565
QY 567 TFGKRLFFYRPSWSKLSIGIRQLKRVQURELSEAEVQRHARALTSRLRFTPK 626
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 566 AKEXQRIFFYRKNIWMNIRLSIDLKQ-NLKQVEXKEMRIJFCESQ-NFADGKRLRIPK 623
QY 627 PDGRLPVMDVYVGARTFRF-----CRARLTSRYK--ALFVLYNEBARRGGLG 677
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 624 GDTFRPLM-----TFNRKIPNQGVRQSGMTNNKLQPAHMLKVLKSRMFKHSFG 674
QY 678 ASVLGLDDIHRMRTFVLVRADPPPELYFVKVDVTGAYDTIPDDRLEVIAS----- 731
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 675 FAVFNDDIMKRYENFVQKK-QINSPKLYFAMDIEKCYDNDVCERVVNPLOKSDLMDK 733
QY 732 -----IKPQNTYCVRRYAVVQKAAGHVAKFAKSHVSTLTDLPTRQVVAHLOET 783
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 734 EYFLNLTFLVKRKNIIVERSNRKLPIQYFRYXQK-IGIDGSSYPLFLIEDDEFND 792
QY 784 SPLRDAVTEGSSILNEASSGLFDVLFEMCHAVIRKGSYVQCGIPQGSILSTLLCS 843
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 793 LNKKRTIIVQEOQRKFPKNDLQPLKICNNYVFNKKQYKQKMGIPQGLCVSILSS 852
QY 844 LQYGMENKLPAGIRD-----GLLRVLDDELIVPHLTHAKTFLRLTVRGVPEY 894
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 853 FYVANEENALQPLRKESMDPEKEINLMLRLDLDLITTKXNMALPIEXLYQSLGN 912
QY 895 GCVVNAKTVNPFVEDEALGFAFVQ--WPAHGFPWCGILDTFTLEVDGSSYAR 951
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 913 FPKFNMKMLKTNALMLQKIGCTNTTQDIDSLNDLPHHIGISIDIKTLNITQNIKKE 972
QY 952 TSIRASVTFNRFKXGRNR--MRKLFQVLRKCHSLFLDLOVNSIQVCTNIYKILLIQ 1008
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 973 GIL---CLVNNQNTESILMLKKLKSFL-MNISFYKSTINTKQFANITLSKLYIA 1028
QY 1009 AYRFHACVQLP-FHQ 1023
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1029 AERYVACCGEPRKPFHE 1044

RESULT 5
Telomerase (EC 2.7.7.-) catalytic chain p133 - Tetrahymena thermophila
N/Alternate names: telomerase reverse transcriptase
C/Species: Tetrahymena thermophila
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14891
R: Collins, K.; Gandhi, L.
Proc. Natl. Acad. Sci. U.S.A. 95, 8485-8490, 1998
A/Title: The reverse transcriptase component of the Tetrahymena telomerase ribonucleoprotein
A/Reference number: Z18252; PMID:98337941; PMID:9671704
A/Accession: T14891
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1117 <COL>
A/Cross-references: UNIPROT:O77448; EMBL:AF061284; NID:93335166; PID:93335167; PIDN:AA03;
C/Genetics:
A/Gene: TERT
A/Genetic code: SGCS
C/Keywords: nucleotidyltransferase
Query Match 6.0%; Score 357; DB 2; Length 1117;

```

Best Local Similarity 20.1%; Pred. No. 3,9e-16;
Matches 192; Conservative 160; Mismatches 369; Indels 234; Gaps 35;

```

QY 322 PPTVATKTHLYSSGDEKQRLPSPFLSSLRPSLTGARRLVETFLGSRPMPTGPRRLR 381
DB 239 PGVF-KSFFNY-----EIKQGFQFVIOEKIQGRQ-----FINSDKIKPHDPQITIK 286
QY 382 -LPOFY-----WQVRPLFLS-----LIGNHAQCPYGLTKHCPPLRAAVTAAVCAR 428
DB 287 KTLKXEQSNFSCQERDLFLETETKIVQNFHININNYLLKFCYL----- 333
QY 429 EKQGVAADEEDTDRRLVQLRQHS-----SPWQYGFYRACL 469
DB 334 -----PENQSLKSVQKQIVQSENKANQSCENLFNSLYDTETSLYKQINFLRQIT 384
QY 470 RLVPPLGWSRNERERFLNTKKETSLGKHALSLQELTWKMSVPCAMRLRSPVGCY 529
DB 385 QNCPVNOVLGKK-NFKVFLKLYEFVQMKRFENOKVDVYCFMDVPQVWF-----V 435
QY 530 PAAEHRL-----REELAKFLHMLMSVYVELRSPFYVETTFQKRLFFYRPSY 580
DB 436 DLAKQKFTQKRYISDRKILGLIVPIINKIVIPLRVYFITEKHKGSGQIFYYRKP 495
QY 581 W---SKQSIGI-RQHAKYQRLSEAEVQRHREARPALTLRLRFFIPKPDGLRITVM 636
DB 496 WKLVSKLTVLKEENLEKEEKLIPEDSFQYPO-----GKLRIPKKGSRPIM-- 546
QY 637 DYVVGARTFRREKAERLTSRYKALFS-----VLYNERARRPGLLGASVGLDIDHRAWT 692
DB 547 -----TFLRKQKQXIKILNINOILMDSQVLRNKLMDLQKIGSVFNKQISKFPQ 599
QY 693 FVLRVRAQDPPELYEVKVDVTGAYDTIPDDRLETVASITIKQNTYCVRRVAVQKAAH 752
DB 600 FIEKWKXKG-RPOLYVYVTLIDIKKCYSDIDQMKLNFENQSDLLQDTYFIKYLFLQNRK 658
QY 753 GHVRAKFSVSTLTDQ-----PYV-----RQFVAHQE----- 782
DB 659 PLIQIOQTNNLNSAMELEBEKINKKPPKMDNINPFYFNLKERQIAYSLYDDDDQLQNG 718
QY 783 -----TSLRDVAVIEQSSSLNEASGLFDFELRPMCHAVRIRKSVYQCGIIPQSIIS 838
DB 719 FKXIQSDRPFIYINQKPRCITFDIHHNLKHAISQNVNISFKVPRQKRGIPQGLNIS 778
QY 839 TLICSLCYGMENKLPFAGIRPD-----GLLRVDDFLVTPHILHAKTFRITLVRCV 891
DB 779 GVLCSFYEGLEEBEYQFLKNAQVNGSINLLMELTDDYFLISDQONALNLTIVQLQNC 838
QY 892 PEGCVVNLKRTVNV--FPVEDALGTAFCVMPAHGLFPWCGLLDTRTLEVOSSY 949
DB 839 NNGGFMNDOKITTNQFPQEDYNL---BHFKISVQNECQWIKSISDMNTLEIK---SIC 892
QY 950 APTSRASVTFRNGFAGANRRRLFGVLRKCHSLFLDI-----QVNSLOTVCNTNY 1002
DB 893 KQYQOEINQITINVAISI-KNLKSQLNKRLR---SLFNQOLIDYFNPNINSFEGLCROY 947
QY 1003 ---KILLQAYRPHACVLOL-----PFHQVWK---NPTFFLRVSDTAS-----LCY- 1044
DB 948 HSHKATYMKFYPMYTKLPQIDLKSKQYSVQYKRENTNENFLKQIDLYYVEDYCKLCTL 1007
QY 1045 -----SILKANAQSLGAKAGAPLPSEAVQWMLCHA 1077
DB 1008 QFEDAINSNIKEIKNLYSWIMMDIIVSYLKKKKQ-----FKGYLXKL----- 1050
QY 1078 FLKLTIRHRTVYPL-LGSLRTAOTOLSRKLPQTITLTALEAANPLPSDFKITL 1131
DB 1051 -LQIKRSRFFYTLKEGCKSLQILISQOKYQLNKKELEAFIDLNNDIQDIKTLI 1104

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RESULT 6
S53396
telomerase catalytic chain EST2 - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein L8543.12; protein YLR318w
C:Species: Saccharomyces cerevisiae

C>Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C/Accession: S53396
R/DU: Z.
Submitted to the EMBL Data Library, February 1995
A:Description: The sequence of S. cerevisiae cosmid 8543.
A:Reference number: S53396
A/Accession: S53396
A/Molecule type: DNA
A:Residues: 1-884 <DUZ>
A/Cross-references: UNIPROT:Q06163; EMBL:U20618; NID:q2258165; PTD:g662136; GSPDB:GN00011;
A/Experimental source: strain S288C (AB972)
C/Genetic: S.
A:Gene: SGD:EST2; MIPS:YLR318w
A/Cross-references: SGD:S0004310; MIPS:YLR318w
A/Map position: 12R

Query Match 6.0%; Score 355.5; DB 2; Length 884;
Best Local Similarity 22.1%; Pred. No. 3.6e-16;
Matches 167; Conservative 127; Mismatches 309; Indels 151; Gaps 28;

```

QY 329 KHFLYSGDKXQLRPS--FLSSLRPSLTGARLV---ETIFLGRPMPTGPRRLRPLP 383
DB 165 KQFLH---KININSSFFPYSKILPSSGSIKLTDLREALF-----PITLVKIP 230
QY 384 QRYWQMRPLFLS-LIGNHAQCPYGLTKHCPPLRAAVTAAVCARREKQGVAADEED 442
DB 231 QRLKVRINLTQKILKRRKRLNLYVLSINSCP-----PLEGTVL----- 269
QY 443 TDRRLVQLRQHSAPWQVGVFVACRLRVLPPGLGMSRHRERPRTRTKKFISSGKAK 502
DB 270 ---DLSHSRQ-SKEKVLKFIYIYIQLKLPQEMFGSKKQKGIKYNLNLISPLNGY 324
QY 503 LSLQELTWKMSVPCAMLRSPGVGCYPAAEHRL--EELAKFLHMLMSVYVELRSP 560
DB 325 LPFSDLLKRLKLDPRWL---FISDIWFTGHNENLNQALICFISLWFLQRLIKIQT 380
QY 561 FYVETTFQKRLFFYRPSVSKQSIGIRQHLKRVQRLSEAEV-RQHREARPALTL 618
DB 381 FYCEIS-STVTIVFRHDVKNKLTIPRIVEYFKTY---LVENNVCNHSYLSNENH 435
QY 619 SRLRFPKPDGLRPVNDYV-----GARTFRREKAERLTSRYKALFSVLYNERAR 672
DB 436 SKKRIIPKKS-----NNEFRILAIPCRGADBEETIYKHNKQALQPTQKILEYLRK 489
QY 673 PGLGASVGLDIDHRAKRTVLRV--RAQDPPELYEVKVDVTGAYDTIPQDLTEVIA 730
DB 490 PLSF-TKLYSPLOADR-LKEFKORLLKFNVLDELFFMKFDVKSQYDSIAPRMECRLIK 548
QY 731 SLIKPQNTYCVRRVAVQKAAHGHVRAKFSHVSTLTDLPQYMRQFVAHLOETSPLRDAV 790
DB 549 DALKENGFYRSQYFEN--TNTGYLKL-FNVNARSRPKY-----EL 589
QY 791 VIEQSSSLNEASGLFDFELRPMCHAVRIRKSVYQCGIIPQSIISLTLCSLCYGM 849
DB 580 YIDNVRTVHLNQDVINVENMEIEFTALMVEDCKYIRBEGDFQSSSSAPAPIVDYDDIL 649
QY 850 --ENKLFAGIRPDGLLRLVDDPFLVPHLTHAKTFRITLVRCVPEYGCVNLRKTV-VN 906
DB 650 EYSEFKAPSGQDTILLADPFLISTDQOQVINIKKLAMGFGQKYNAKANRDKILAVS 709
QY 907 FPVEDALGTAFCVMPAHGLFPWCGLLDTRTLEVOSSYVARTSIRASVTFRNGFA 966
DB 710 SQSDDDT-----YIOFCAMHI FVKELEWGHGSSSTNNFHIRS-----KS 748
QY 967 GANMRKILFGVLRKCHSLFLDLOVNSLOTVCNTN-----YK-----ILLQ 1009
DB 749 SKGIFRSLIAFNTRISYKTDINNSNTVLMQODHYVKNISBQYKSAFPLDSINVTQN 808
QY 1010 YRFACVQLPFHQVWKRPFFLRVISDTSALC 1043
DB 809 MQFH-----SFLQRIIEMTVSGC 826

```

RESULT 7

A59266
 unconventional myosin-15 - human
 C/Species: Homo sapiens (man)
 C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C/Accession: A59266
 R/Jiang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Man, T.B.; Friedell, R.A.
 Genomics 61, 243-258, 1999
 A/Title: Characterization of the human and mouse unconventional myosin XV genes responsible for deafness
 A/Reference number: A59266; MUID:120021762; PMID:10552926
 A/Accession: A59266
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-3530 <LIR>
 A/Cross-references: UNIPROT:Q9UNX7; GB:AF144094; NID:66224682; PIDN:AA05903.1; PID:66224682-1867/Domain: myosin motor domain homology <MMO>

Query Match 2.9%; Score 175.5; DB 2; Length 3530;
 Best Local Similarity 20.4%; Pred. No. 0.0048;
 Matches 260; Conservative 145; Mismatches 394; Indels 475; Gaps 67;

QY	107	AGGPEAFTS-----VRSYLP-----	NTVTALRGSGAWG	138	
DB	2313	SRGGKVVGVGNSWSDSDMSTPQPOEHWKVLSDGSSHNQDGTNETEAKGT	ATH	2371	
QY	139	LLRRVGDVVLHLLARCALFVLVAP-----	SCAYQVCGPLYQLGAA	181	
DB	2372	QESDSLGEPAVPHKGLDYLDFPVLISYGDADLEKFTALAYRMKGGCGGSGSGTE	2431		
QY	182	-QVAPP-----PHASGRRRLGGERAMNSVRAGV---	PLGIPAGARRGSGAS	RLSP	233
DB	2432	DTPRRPEPEKFIPLGLDASTLALQCAFH--	KQAVLLARGMTLQAVALLQOPLSALRLSP	2489	
QY	234	LPKPRRGAPEPPEPTPVQSGMAHGRTRGSDGFCVSPAPAEATELEGALSGTR	293		
DB	2490	AEKRP-----APBAQPTSVGTGPAPVLLR-----	ATPKPLAA	2524	
QY	294	HSHPSVGRHAGPSTSPRPMDTPEPVYA-----	ETKHFVSGDYEQLRPSFL	347	
DB	2525	-----PLAKAPRLPIKPVAAFLAODQASPET-----	TSPSELVAYSTLN	2565	
QY	348	SSLRLPGLGARLVETIFLGSSPMWGPGRRLPLPFRWQWRP-----	LFLELGNH	400	
DB	2566	SEHFPPT--QQTIVRQYQCPFGGRPEALRKQGVKMKRPPHEALMLKGVTH	2623		
QY	401	AACPVG-----VLK--THCPRAAVTPAAGVCAREKPGSVAAPEE	EDTDPRLV	449	
DB	2624	LAAPGTQVSRBAVALVKEVTSAP--RPSWAPTSAL-----	PSRSLPEBELTQTLHRLI	2677	
QY	450	QLRQHSSPMQVGVGR-----	ACLR-----RL	472	
DB	2678	NPFVGYQAPWKT--FLRKEVFYPRDSYHPVQDLDFRQILHDTLSEACRISSEDERL	2735		
QY	473	VPPGLMGRHNRERFLNTRKFEISIG-KIAKLSLOELTWKMSVSDCAMLRRSPGVGCPVA	531		
DB	2736	RKALFAQNO-----LDTGKPLVTSYKRAVASTARDTWEV-----	YSRFRPATGSGT	2785	
QY	532	AHRRLREELIAFLKMSVYVELLR-----	SFYVETTF-QQNR	572	
DB	2786	G-----VQLLA-----	SSHVGIKLRWKVGGQGAAGQLRVLRAYSFDILFVTMPSQM	2834	
QY	573	LEFPYRVSWSKLQSIGIFQHLKRVQLREISEAEVQRHEARPALTSRLRFLPKDGRP	632		
DB	2835	LEFNLAS--EKVILFSARH-----QVKTLVDFFILELK--		2867	
QY	633	INMDYVVGARTFRRRKRAERLTSVKALFSVLTNERA-----	RRPGLLAGS-----	679	
DB	2868	--DSDVVAVVRNLFLEDPDPA-----	LLAFHKGDIHLQLEPFRVYSGAGCVAR	2913	
QY	680	--VLGIDDIHR-----AMRTFVLAVRAQDPPELFFVKVDVTAQD-----	TIP-QDRLT	726	
DB	2914	KXVYVLEELRRRGPDRGMRFGTIHGRVGRFSEL-----	VQPAADDFQLPTPERGAA	2969	

QY 727 EVASIIKPNQNTVCERY-----AVYQAAHGVKAKAFSHVSTLTDLQPYMRQFVAHLQ 781

DB 2970 AVAAAVASAAAGVGRBRGPPVRAARSADHGEDALALPPY--TMLEPAKVFEDDPRRQ 3028

QY 782 E-----TSPLRDAVIEGSSSINEASSGLFDFVLRPMCHAVR 819

DB 3029 DGLRKSKEPREERTLEDMLCFTKPTLOESLIELSDSSISKMATDMLFVAFMFGMDAPLK 3088

QY 820 IRKSVYQCGGIGQSSILSTLCSLCYSD--MENTLFNGI-----RRDG 861

DB 3089 GQSDLDVLN-----LTKLC-GHEVNRDECTQVQKQITDNTSSKQDSQGRW 3136

QY 862 LLRLVYDF--LVTPLHTAKTFLRLVR--GVPEYG-----CVNLRKTVAFPVED 911

DB 3137 RLVIYVTAHSGSEVLAHPHLR--FLQVSRPPGFQGIKACRONLQKTL----- 3186

QY 912 EALGGAFFVMPAHGLFPMWGLIDRTLEVGSDYSYARTISRAVYTNRRGKAGNR 971

DB 3187 -RRGG-----RLPSSIEU--RMLAGRSSK 3210

QY 972 RKLFF--GV--LRKCHSLFLDLQVNSLQTVCT-----NLYKILLQAVRFA 1014

DB 3211 RQLFLPGLGERHLKTKCTVALDV--VEEICAMALTRPBAFNEYVIFVYTRNGCHV 3266

QY 1015 CVL-----QLPFRQVWKPIFF-----LRVSDTHSLCY 1044

DB 3267 CPLSRRAIYLDVASEMEQYDGYMFWFRVLDQPLKFENEDLYTMHVNQVLDLKLGF 3326

QY 1045 SILKAKNAGSLAKGAGPLPSEAVQWLCHOAFILKTRHVT--YVPLGSLRTAQ- 1100

DB 3327 SSVPASR-----PSEQ--LLQVSKLASIQHAKHFIPL--SVREYGE 3366

QY 1101 --TQSLRKLPQGT 1111

DB 3367 YIPALYRTTAGST 3380

RESULT 8

Q0353
 BHLF1 protein - human herpesvirus 4 (strain B95-8)
 C/Species: human herpesvirus 4, Epstein-Barr virus
 C/Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
 C/Accession: A03742
 R/Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barber, B.G.
 Mol. Biol. Med. 1, 21-45, 1983
 A/Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus.
 A/Reference number: A93065; MUID:85035713; PMID:6092825
 A/Accession: A03742
 A/Molecule type: DNA
 A/Residues: 1-660 <BAN>
 A/Cross-references: UNIPROT:P03181
 R/Baker, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; He Nature 310, 207-211, 1984
 A/Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
 A/Reference number: A03794; MUID:84270667; PMID:6087149
 A/Contents: annotation; protein coding region
 C/Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-523; Superfamily: human herpesvirus 4 BHLF1 protein

Query Match 2.9%; Score 172.5; DB 1; Length 660;
 Best Local Similarity 26.1%; Pred. No. 0.00077;
 Matches 94; Conservative 16; Mismatches 159; Indels 91; Gaps 16;

QY	167	AYQVC--GPEVLQATQA--RPPHAGPRRRGCEBAMNHSVEAGVPLGPAPGAR	222	
DB	244	AAQRCAPGPPPTTSGAAQTRRRPFCRSANBECPTWR--RSGAQGHPPFGAG	300	
QY	223	RRGASRSRLP-LPKRRGAABEP-ERTPVQSGMAHGRTRGSDRGFCV-VSDAR--	277	
DB	301	QRRSGPTGRPAAPGAPTPAPGPGGAAPVSGATPHERRSGPADPAPAAALPEROE	360	
QY	278	-----PAEATSLGAL-----	SGTRHSPR	297

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Db      361 PRLEQDLAAQRCRCPPTRRSGAAQRTTRPPGCRSARNPCCRTMRRRSGAQRGP 420
Qy      298 SVGRQHAGPPSTSRPPRPW-DTPCPP-----VYATKFLYSSGDKE-----QJR 342
Db      421 PPGAGGRRPGSGPTGRRPAPGAPGTAPAGPGGAAPVSGATPHRSGSGPADPPAARLP 480
Qy      343 PSFLSLRRSLTGARLVETITLGSRPMPG-----TPRLRLQ-----RYWQM 389
Db      481 PERQEPRLPDLLAAQCP-----AGPPTRSGAAQRTTRPPGCRSARNPCCPTMR 536
Qy      390 RPLLELGNHAOCPPYGLKTHCP-L-RAAVTPAAVCAREKPGSVAAPEEDTPRR 447
Db      537 RS-----GAQRGHPPAPGAGRRPGSGPTGRRPAPGAPGTAPAGPGGAAPVSGATPHR 591

RESULT 9
T00080
hypothetical protein KIA0522 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00080
R:Ngasee, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kocani, H.; Nomura, N.; Chata, O.
DNA Ref. 5, 31-39, 1998
A>Title: Prediction of the coding sequences of unidentified human genes. IX. The complet
A:Reference number: Z14086; MUID:98290545; PMID:9628581
A:Accession: T00080
A:Molecule type: mRNA
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-1560 <NAG>
A:Cross-references: UNIPROT:O60275; EMBL:AB011094; NID:93043567; PIDN:BA25448.1; PID:93
A:Experimental source: brain; clone HG1393
A:Genetics:
A>Note: KIA0522

```

```

Query Match      2.4%; Score 142.5; DB 2; Length 1560;
Best Local Similarity 29.5%; Pred. No. 0.28;
Matches 65; Conservative 15; Mismatches 89; Indels 51; Gaps 12;

```

```

Qy      173 PPIYQALQAPPPHSGPRRLGGERAMNSVREAGP-----LGTPAGARRRG 226
Db      1365 PPIYQALQAPPPHSGPRRLGGERAMNSVREAGP-----LGTPAGARRRG 226
Qy      227 SARRSLPLRRP-RKGAAPPEPTPVGQGSMAHPGSTRGSDRGFCVSGPAPPAEATSL 285
Db      1416 GHDQAFPHGHPLHOPISPLPLYSPPAPQHPAH---KQPKHPIFGHHPQMPMAAGMAG 1472
Qy      286 EGAL-SGTRSHSPSVGRHAGPPSTSR---PPRPMDTPCPPVYAETKHF----- 331
Db      1473 PGRPRPGGSGSHR-----HHQSPPLSPHSHIPPHSPPLPPSPPTTPSPPLPPTSPHGP 1527
Qy      332 LVSSGDKQLRPSFLISSLRPSLTGARLVETITLGSRPW 371
Db      1528 LHASGPPAQTPP-VQTPRPSQA-----GSAPW 1554

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```

RESULT 10
T18314
hypothetical protein L7610.4 - Leishmania major
C:Species: Leishmania major
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18314
R:Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rejandream, M.; Ivens, A.;
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18876
A:Accession: T18314
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1892 <OLI>
A:Cross-references: UNIPROT:O97007; EMBL:AL034356; NID:e1371878; PID:e1371559; PIDN:CAA2
C:Genetics:
A>Note: L7610.4

```

```

Query Match      2.4%; Score 140.5; DB 2; Length 1892;
Best Local Similarity 23.4%; Pred. No. 0.5;
Matches 111; Conservative 47; Mismatches 195; Indels 121; Gaps 25;

```

```

Qy      44 PAARFALVAQCIVCPMDARPPAPSPFQVSCIKELVARVQLRCERGANVLAFGPAL 103
Db      366 PSLHLPQQQPIVILVP---QPRPAPQOERLPRLYSSSTRRAGGSRAPVNNIYAGDA 422
Qy      104 LDGAGCPPEAFATTSVRS-----VLENTVDALRSGAGMILLRRVGDVVLHLLRCA 158
Db      423 EDTSSGAEVSTSTRSRTQVRRAPVYASDIPGS--PYGM-----PT 465
Qy      159 FVLVAPSCAYOCGPVYQLGATGARPPHAGS---PPRLGQ-----ERAWN 204
Db      466 YAVVMPQ--RSLPAPFKTASAGLPPSPAPPAQAQPOHNSRCPPSSSRPQESRD 523
Qy      205 HSRERAGVPLGLPAGAR-----RRGSASRLP---LPKRP--RGAAPPEPT 249
Db      524 HAAREQ--PLPQPPQKRPALPQRHQPQRAETAKSQLEPPMRRLPADPYSSEILPEQRR 580
Qy      250 PVGQSSMAHPGRTGSDNR-GPCVSPARPA-----EATSLGALSGTRSHP-SVGRQ 302
Db      581 --EGAWDGNASTQSGHGRGSHVVRPSQQLSLSHEDLSLAMLSTAVTAATISTKTD 637
Qy      303 HHAGPSTSRPPRPMDTPCPPVYAETKFLYSSGDKEQLRPSFLISSLRPSLTGARRL-V 361
Db      638 PYAGHTADGSRPLHVMVPPPIIQRP--YAATEEE-----GAPRRSV 678
Qy      362 ETIFGSRPMMPGPRRLPRLPQRYWQMRPLFELGNHAOCPPG--VLKTHCPRLAA- 418
Db      679 RKVTAPQESDAPSGRHP-----PAEHTLLSRGAADGAAAKTRQLSLAK 728
Qy      419 ---VTPAGVCAREKPO-----GSVAPEEEDTPRRLVQ---LLRQSSP 458
Db      729 EAVTAMTAVGQSSKRRQLOHEPDGS---PNGDDVD--ELLEADDLIMQSRP 777

```

```

RESULT 11
EBB31P
Immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser)
C:Species: suid herpesvirus 1
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: S04713
R:Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
A>Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies vi
A:Reference number: S04713; MUID:89315207; PMID:2546124
A:Accession: S04713
A:Molecule type: DNA
A:Residues: 1-1460 <CHB>
A:Cross-references: UNIPROT:P11675
C:Keywords: DNA binding; early protein; transcription regulation

```

```

Query Match      2.3%; Score 140; DB 1; Length 1460;
Best Local Similarity 24.3%; Pred. No. 0.38;
Matches 114; Conservative 35; Mismatches 163; Indels 158; Gaps 27;

```

```

Qy      46 AFRALVAQCLVCPMDARPPAPSPFQVSCIKELVARVQLRCERGANVLAFGPALD 105
Db      704 ACRGVLRLPLPC-PLRPPAPARAPALQACLEVTALL-----ALRD 746
Qy      106 GARG-GPPE-----AFTTSVRSYLPINTVDALRSGAGMILLRRVGDVVLHLLAR 155
Db      747 AIPGAPRQQAADSVALLVARTVAPLVRSVQDARAREAAW-----TYA 791
Qy      156 CALFVLVAPSCAYOCGPVYQLGATGARPPHAGS---PPRLGQ-----S 206
Db      792 AALF---APA---VYAGRL---AQAARPGAPRAP---GLPPLMPDQGLVAPAPA 837
Qy      207 VREAGVPGLPAPG---ARRRGSASRSLPLRPPRGAAPPEERTPVGQGSMAHPGRT 262
Db      838 PAAAGAPSGLPGSPSSPASTKSGSTKSSGSGTSGLSGSS-----GYARLRPR 887

```

QY 263 RPSDRGFCVSP---ARF-AEFAISLEG-ALSGTSHSPSVGRQHNAHPSTSRP-- 313
 DB 888 PPSASAAQEEAFRAGARPGEDEEGISGALGDGHRD--DEDRPRRRKRSLG 945
 QY 314 --PRMDTPCPVVAETKHFIVSSGDKQLRPSFLLSLRPSLTGARLVETIFLGSRPW 371
 DB 946 LQPAF--DPAPALVSSSS--SSSEDDRRLR-----RP-----LGRNPE 980
 QY 372 MGTPLRLRLPQRYWQMRPLFLELGNHACQCYVLKTHCP-----L 415
 DB 981 HPAAPDGGFRVDPAG-----ETHPRPSAAALAAAYCPREVALVDQEVPELW 1028
 QY 416 RAAVT--PA--AGVCAREKQGSVAAPBEDTDPRLVQLLRHSSPMQV 461
 DB 1029 RPAITFDPAALAHIAAR--RGAAGP-----LRRAAMRQLADPADV 1069

RESULT 12

AS59295
 Unconventional myosin-15 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C/Accession: A59295
 R/Liang, Y.; Wang, A.; Beljantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Mian, T.B.; Fridell, R.A.
 Genomics 61, 243-258, 1999
 A/Title: Characterization of the human and mouse unconventional myosin XV genes
 A/Reference number: A59295; MUID:20021062; PMID:10552926
 A/Accession: A59295
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-351 [L1A]
 A/Cross-references: UNIPROT:Q9QZ24; GB:AF144095; NID:96224684; PIDN:AAF05904.1; PID:96224
 C/Genetics:
 A/Genes: MGI:Myo15
 A/Cross-references: MGI:1261811
 A/Map position: 11:33.9
 F:1209-1871/Domain: myosin motor domain homology <MMO>
 Query Match
 Best Local Similarity 17.6%; Score 140; DB 2; Length 3511;
 Matches 189; Conservative 115; Mismatches 387; Indels 380; Gaps 44;

QY 3 RAPRCRAVSLLRSHYEVLPATVFRRLGPGQWRVGRDPAFRAVLVQCLVCP-- 59
 DB 677 RPPRLASPYGSLRQH-----PPPW-----AAPAHVPFPQA 707
 QY 60 --WDARPPRA-----PSPRQVSCIXELVARVLQSLCRGAKNVLAFGFA 102
 DB 708 NMWGFAPDPTGSEVAAPDLAPVPRPFR-----ASRSSRRAAYGFP 751
 QY 103 LLDGARGPPEAFITTSVRSYLPTVTD--ALRGSGAMGLLRVGDDVILHLLARCALFV 160
 DB 752 -----SPSLIGSRRLPRLSPQSLRSLDGG----- 778
 QY 161 LVAPSAVQVCPVYOLGAATCARPPRPLASGPRRLGGERAMNSVREAGVPG-- 215
 DB 779 -----YHSPILPLSFLSLRGRPPQPPPPRRPQSLREAF--SLRPSGRLLPPSP 830
 QY 216 -----LPAPGARRRGSGASRLPLPKR-----PRKGAPEBERT--FVGGGS 255
 DB 831 VLGSPRPSPPLPKGPRHRSILNPSRLPRTWRRLSEPTTAVVPMWRAPVPPSPSGP 890
 QY 256 MAHPGTRGSDRGFCVSPPARPAEATSLGALGSTRSHSVGRQHNAHPSTSRPR 315
 DB 891 W--GASTGALD-----QOENQREADESETPVPLAPSMVDVMPQRPSP 935
 QY 316 PMDTPC-----PVVAETKHFIVSS--DKEQRLRPSFLS 348
 DB 936 PMBEGISLGRSPRPVPEPNLEHTSCEPQSEDRSVNLTGIFLQGHDPGCGULTX 995
 QY 349 SLRPSLTGARLVETIFLGSRPWMPGTPRRL--PLRQRYWQMRPLFLELGNH----- 400

DB 996 SADPSL---EKPEVVTLLD--PQPAPEPALPTPPNKNVAVSERKVLRLASAYPLVTCQ 1051
 QY 401 --AQCP-----YGVLLKTHCPPLAAVTPPAAGVCAREKQGS----- 434
 DB 1052 ARATQWQMRKWKVSTPAPLPTPAAPGLLKGQSPRAEPGRFAVVMQVGVSSFRPK 1111
 QY 435 ---VAPEBEDTDPFR-----LVOLLRQSSPMQVGFVPAAC 468
 DB 1112 GPAVPQEPHPDPPQGPAPQACSLRWCPLMPPTDNLHGLWRIRITYSQSLRHGGDC 1171
 QY 469 LRRL--VPPGLWGSNHNERRPLRNTKFTISLQKAKLSQLLTKWMSVRCAMLRPSRG 525
 DB 1172 HXSLMKTRPSQV---QNGKHSIRNLPSMRSEQHREDEVMOTLEDLQETTVLAN-- 1225
 QY 526 VGVPAAEHRLREILAKFL-----HWLMSYVVELLSF-----FYVT 564
 DB 1226 ---LKTRENNLYTYTIGSLVSVMYRKFAIYGPQVOQYGRALGENPHLFAA 1279
 QY 565 EITFOR-----NRLFYRPSVMS-----KL-----QSIGRQLKRVQLRELS 603
 DB 1280 NLAFAMDLAKQNCQVIGSGSGSKTEATKILRGLAMNQRPVMOQIKILEATPLIE 1339
 QY 604 A-----EYQHRARARALLTSRLRFTPKPDGLRPIVMQYVGARTFRERKAER----- 653
 DB 1340 AFGNAKTVRNDSSR--FGKFEVLEPGVIGCAITSGQYLEKSRIVFOAKNENYHIF 1396
 QY 654 -----LTSRKALFSLVLYE-----PARRGLGASVGLDDIHRANRTVLRAQD 701
 DB 1397 YELLAGPLRQAFSLQZEAFETYVLYNQGNCSEIAGKS--DADDFPR----- 1441
 QY 702 PPELVFVKVDVTAADTIPQRLTFLVLSITIKPQNTYCVRRYAVQKAHGVKAFKS 761
 DB 1442 ---LAAAEVLG--FTSDDQSIIFRLASIHLAGVYKEKETDAQEA----- 1485
 QY 762 HVGTLTDLPYMQFAHLOETSP--LRDAVYIEGSSSINEASGLFVFLRFMGHAYR 819
 DB 1486 SVASABEIQ-----VAELQVSPBGLQALIFKYLETIRE-----KIFTLVYESAID 1534
 QY 820 IRKSYVQCCGIPQSGISLTLLCSLCYGMENKLFPGI--RQDGLLRBYD 868
 DB 1535 AR-----DAIAKVALLFGWILIRVNAVSPKDDTLIALID 1572

RESULT 13

F75311
 ABC transporter, ATP-binding protein - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: F75311
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: F75311
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-552 <WHI>
 A/Cross-references: UNIPROT:Q9RS9H; GB:AE002048; GB:AE000513; NID:96459929; PIDN:AAF1168
 A/Experimental source: strain R1
 C/Genetics:
 A/Genes: DR2145
 A/Map position: 1

Query Match
 Best Local Similarity 22.3%; Score 139.5; DB 2; Length 552;
 Matches 134; Conservative 38; Mismatches 196; Indels 233; Gaps 27;
 QY 132 RSGAGWGLLRVGGDVILHLLARCALFVLVAF-----SCAYVQCP 173
 DB 24 RGS---RLQFRVSGKSTRIRFTSTESLFLCLARLGLTASSTGSIHSSDVATTAAPRP 80

QY 174 P----LYQLGATQAPPPHAGSPRRRLG-----C 199
 Db 81 PGTNRHRRRGAG--AARPPFADGPARRGAAAGERRRRONHAAAAARACASERHPDV 138
 QY 200 ERAMNHGVREAGVPLGLPAGARRRGASASRLPLPRPRRGAPRPERPTVQGGANP 259
 Db 139 ARRGSGAFRRAGA--AIPERGAGRRGVLSRLGTDPRARAAAGRGRTPAVGSDA-- 194
 QY 260 GRTGSPDRGFCVVSPPARPAEATSLGQALSGTRHSHPSVGROHACPPSTSRPPRPMDT 319
 Db 195 -RTTRPVGRG-----DYTRRGALAGALSHPLA---RAAPFGDAGP----- 232
 QY 320 PCPPVVAETHHFLVSSGDXQLRPSFLSSLRPSLTARSLVETIFLGSFPMWPGTPRRL 379
 Db 233 -----RPDARA-----PAAAFRI 246
 QY 380 PRLPQRYWQMRPLEL---LGNH-----AACPYGLLKTCPRAAVTPA 422
 Db 247 HRNPERSGPRPRRRARAPGCGHGVGADPPARGSPDALAGVNSGRTERRAALPI 306
 QY 423 -----AVCAAREKQGSVAAPDEEDTD-----PRLVOLLRQHSSPMQV---YGF 464
 Db 307 RSPRYSGASTGPLCGTALVELTDAEVPFRNGHRLGLPMTWAAGH---WLVTEGNS 363
 QY 465 VRACLRRLVP-----PGLMGRHNERRFLRNTKFKTISLGHAKXLSLQELTWKMSVRDC-AM 519
 Db 364 GKSLTALILAGELHPLAGGS--VARPL-----ARDVQGS 396
 QY 520 LRNSPGVGVPAAEHRLREELTLAKFLHMLSYYVELLSFFVYTE-----TFQKRLP 574
 Db 397 RRRRTG---LVSAEAVGIRORSVSGREMLGR---DVIASAFGTBGTGDTVAEQ----- 445
 QY 575 FYRPSVSKXQSGTIGR-----QHLKRYQLRELSAEVRQREARPALTLRLRP 623
 Db 446 -----MDAVGTLAERLELGBELLSDVQALSQGLRLLRLAARVH-PRLLLDLGLDF 498
 QY 624 I 624
 Db 499 V 499

RESULT 14
 S27923
 gene LF3 protein - human herpesvirus 4
 C/Species: human herpesvirus 4, Epstein-Barr virus
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S27923
 R/Parker, B.D.; Bankier, A.; Satchwell, S.; Barrell, B.; Barrell, P.J.
 Submitted to the EMBL Data Library, August 1990
 A/Description: Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B9
 A/Reference number: S27923
 A/Accession: S27923
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1924 <PAR>
 A/Cross-references: UNIPROT:Q99307; EMBL:M35547; NID:9330420; PID:AAA5896.1; PID:93304
 C/Superfamily: collagen alpha 1(I) chain, fibrillar collagen carboxyl-terminal homology;

Query Match 2.3%; Score 138.5; DB 2; Length 924;
 Best Local Similarity 27.0%; Pred. No. 0.26;
 Matches 80; Conservative 25; Mismatches 136; Indels 55; Gaps 16;

QY 179 GAATQAP-----PMAAGRRRLGGERAMNHGVREAGV-----PLGLPAPGARRGSA 228
 Db 26 GAADPADPVGHAPAPAPGEPRTRLQPA---TPRSSGAADPADPVGHDA--APRAPGE 80
 QY 229 SSSLPLPKPRRRGAPRERTPVCGGSMARPGTRGSPDRGFCVVSPPARPAEATSLGSA 288
 Db 81 PRTRLQATPRSGADP-ADPVG-----HPAAPAPGEPRTRLQPATPRSGAADPAD 134
 QY 289 LSGTRSHSPSVGRQHAGP-----PSTSR-----PPRPMDTFCPPVVAETHHFLVSSGD 337

Db 135 PVG-----HPAAPAPGEPRTRLQPATPRSGAADPADPVGHAPAP-----RABGP 181
 QY 338 KEQLRPSFLSSLRSLGARGRLVETIFLGSFPMWPG--TPR-RL-PRLPQRYWQMRPLE 394
 Db 182 EPRTR-----LQPATRRSGAADPADPVGHAPAPAPGEPRTRLQPATPRSGAADP--A 235
 QY 395 ELGNHACQPIGVLLKTHCPRLAAVTPAAGVCAAREKQGSVAAPDEEDTDPRRLVQ 450
 Db 236 DVG--HPAAPAPGEPRTRLQPATPRSGAADPADPVGHAPAPAPGEPRTRLQ 290

RESULT 15
 C45219
 N-methyl-D-aspartate receptor chain NMDAR2D-1 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C/Accession: C45219
 R/ishi, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazawa, J.
 J. Biol. Chem. 268, 2836-2843, 1993
 A/Title: Molecular characterization of the family of the N-methyl-D-aspartate receptor su
 A/Reference number: A45219; MUID:93155102; PMID:8428958
 A/Accession: C45219
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-1356 <ISH>
 A/Experimental source: brain
 A/Note: sequence extracted from NCBI backbone (NCBI:124264)
 C/Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology
 F/451-879/Domains: glutamate receptor homology <GNH>

Query Match 2.3%; Score 135; DB 1; Length 1356;
 Best Local Similarity 27.2%; Pred. No. 0.76;
 Matches 88; Conservative 16; Mismatches 102; Indels 118; Gaps 22;

QY 59 PWDARPPPA-----PSRQVSCKEIVARVQLRCERGANVLAFGALDQ----- 106
 Db 1084 FRRAAPPCCAYLDLEPS-----PDSSEDSLSLGASIGLEPMWFA 1124
 QY 107 -----ARGPPRAFTTSVRSYLENTVTDALRG--SGAKGLLRRVDDVTLHLARCA 157
 Db 1125 DFPYPAERLGPPEGRTYSV-----DRLGGRASWDYLLPRRGP--AMHCRHCA 1172
 QY 158 LFLVLP-----SCAYQVC-----GPLYQLGATQAPPPHAGSP-----RRRLCGERAMN 204
 Db 1173 SLELLPERRHLSGSHDGLDGGWMAFP-----PPPAAGPPRRRARCGCPRRHP 1221
 QY 205 HSYREA-GVPLGLPAPGARR--GG-----SASRL-PLPKPRRGAAPEPRT-PVG 252
 Db 1222 HRPRASHRAPAAPRRHHRRAAGGWDPPPAPTSRSLIEDLSNP---CP-PHRTGDTG 1276
 QY 253 QGSMAHPRTGSPDRGFCVVS-----ARPAEATSLGQALSGTRHSHPSVGROHHA 305
 Db 1277 AGTAHHAALR-----ISPAHSRYDAAPAPTPRAPPSVA---GHGPRGRAKMT 1324
 QY 306 GPPSTSR---PPR--PMDTPCP 323
 Db 1325 GPSWVGXDRNPGCRTPPGAASCAP 1348

RESULT 16
 G75302
 orotidine 5'-phosphate decarboxylase - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C/Accession: G75302
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S.
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uitterback, T.; Zalewski, C.; Mal
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: G75302
 A/Status: preliminary

A:Molecule type: DNA
A:Residues: 1-606 <WHI>
A:Cross-references: GB:AE002053; GB:AE000513; NID:G645999; PIDN:AAF1749.1; PID:G646000
A:Experimental source: strain R1
C:Genetics:
M:Gene: DR200
A:Map position: 1

Query Match	2.2%;	Score 134;	DB 2;	Length 606;
Best Local Similarity	22.4%;	Pred. No. 0.29;		
Matches 100;	Conservative 45;	Mismatches 137;	Indels 164;	Gaps 21.

```

0Y 132 RGSQMGWGLLRVGGDVLVHLARCALFVLAIPASCAVCGPPLVYUGAAYCARPPHAS 191
Db 21 RRSERFGVALLQIGERRRVHLTAHRPAFLQ-----LGAVER----- 57
0Y 192 GPRRLGGERAMNSVREAGVPLGIPAFGARREGSASRSLPLKRRPRGKAAPR----- 246
Db 58 -PSRRFG-----VGVPVSGGRG-----VLDEQR-----PPFQFVF 91
0Y 247 -ERTVCGGSMANPRTGPSDRGCVVSPAPPAEATLSGALSTGRHSHPSGROHA 305
Db 92 RORT-----GVLPAAKOQ--VKVCGPROFAAGV-GVVYGAQ-VHPVYUGAAYA 136
0Y 306 GPPSTRPPRPMDTPCPPEVYATKHFLLYSSGDKSQLRPSFLSSLRPSLTGARLVETIF 365
Db 137 A-----PRP-----RAQQRRLPPAPVAALVLP--GPORROOT-- 167
0Y 366 LGSRPWMTGSTRRLPLRLPQRYWQMRPLFLLELGNHNAOCQPVVLLKTHPRLBAATPPAGV 425
Db 168 AGEROLTVG-----LPFCPRHV-----QHARPGEDVALNRHHRPREAKRP--GV 209
0Y 426 CAR-----EKPGSVAPAREEDTPRRLTQLLRHSSPMQVGVFYACILR 471
Db 210 AARAGEGALFVRADQEPRLPLVDVGVGLTXAGDDBLRPELRREGQQTFRTEIGVDILNR 269
0Y 472 LVPGLWSSRNERRFLNTKFKFISLGKHAKLISLOELTWKMSVDCANLRSFGVG----- 527
Db 270 YRFPAAHGEGQ-----RPHREILARHDAEVA-----GPVAPHR 306
0Y 528 -----CYPAAEHRLREELIAKFLHW 547
Db 307 KGHARQCTGPAQHPPFVPOLRPLHW 332

```

Query Match 2.28; Score 133; DB 2; Length 1106;

QY 185 RPPHAGSPRRLLCE---EAMNHVVRAGVPLGLPA--PGARRGGSSA-----RSLP 233
 Db 516 RGPQPHGPEPARCRVHRCNHPALARGHGVLLGMAADGPPAADRGGAGAGDGEPXGP
 QY 234 LPKPRFAGGADEPRTVGGGSMANHGRTGSDRGFCVSVAPRPAEATSLLEGALGSTR 293

Query Match	2.2%;	Score 132.5;	DB 2;	Length 946;
Best Local Similarity	20.1%;	Pred. No. 0.68;		
Matches 130;	Conservative 74;	Mismatches 249;	Indels 195;	Gaps 277;

```

Db      576  AGRRPR---VPR-----RAAGRHPLRRG-----ZAHPRGHTDLR---AGSR  613
Qy      294  HSHPSVGRQHNAQPSRSTSRPPRPMWTPCRPVYAETKHFLYSGDKQLRSTLSSLRPS  353
Db      614  PLRR---RAVNHPRAPAGCPRRPRRDPAAGPRQHPRRARARGH---RGGIDRGHPS  668
Qy      354  LTGARRLVETIFL---GSRPMRGTPRRLPRRLQRYQMPLFLLELGNIAOCQYGVLLKT  411
Db      669  RGRYRRRGRAIGLPGSGOGEHNAVHRRLPLRP-----PL-----  702
Qy      412  HCPYRAVTPAQCVA-----REKPGSVA-----APEED-----TD  444
Db      703  HRGGAASRSGEGARLADGPRRPGOEPRGLGPRPAGCPRGGRVRLROYNADQDRPLOG  762
Qy      445  PRLVQLLRHSSPMQYGYFVRACLRLVPPGLMSGRHNERFLRNTKXFLSGHAKUS  504
Db      763  PGQAGACRQARAPRPPRGSTRA-----PGQGGRGSEPH-----RAHATIQ  804
Qy      505  LQELTWKMSVRCAMLRSP--GVGCVPAHEHRLREELIANFLKMLSVYVELLRSEF  561
Db      805  PRHLHGVR-RDPOLALRGDPRGPG-LPAGPYLL-----  837
Qy      562  YVETTFQKRLFFRPSVWSKLSIGIRQHLKRVQLLESEAYVQHREARPALTSRL  621
Db      838  -----QH-----QGRALRGVGRHHEDEDELPAGLL  864
Qy      622  RFI-PKEDG-LRPIVMNDYVVGARTFRREKAER---LTSRKALFSTLANERAPRGL  675
Db      865  RAVAGVRRGVQVEDADAGHLOGOEHNRGPRNADRGGRGLLOVNHPIALRGHARRRSGL  924

```


Db 804 -----LAPCLFYGLVGIAMKSHLNKIRIIOAKTLRISGAPWYMT 846

RESULT 21

immediate-early protein - suid herpesvirus 1 (strain Kaplan)

C/Species: suid herpesvirus 1

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: A45344

R/Vicsek, C.; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzet, M.

Virology 179, 365-377, 1990

A/Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented

A/Reference number: A45344; MUID:91021039; PMID:2171211

A/Accession: A45344

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-1446 <VLC>

A/Cross-references: UNIPROT:P33479; GB:M34651; NID:G334070; PIDN:AAA47470.1; PID:G334071

C/Superfamily: herpesvirus immediate-early protein 1B175

C/Keywords: DNA binding; early protein; transcription regulation

Query Match 2.2%; Score 131; DB 1; Length 1446;

Best Local Similarity 21.4%; Pred. No. 1.6;

Matches 105; Conservative 37; Mismatches 156; Indels 192; Gaps 25;

46 APPALVAGCTVCPMDARPPAPSPROVCLKEIVARVLCERGAKNVLAFGALLD 105

693 ACRGVETRLPC-PLRLPAPAPALGACLEVTALL-----ALRD 735

106 GARG-GPPPAFTTSVRSYLPNTVTDALRGSGAMGLLRVGGDVLHLLARCAFLVAP 164

736 AIPGADPAPER-----ROADSVLA-IVAR-----TVAP 761

165 SCAYVCGEPPLVQLG-----AATQARPPHAGSPRRRIGCERAMNH- 205

762 LVRYSDGAPAREAWTYAALFAPANVAARLAPALPGAPAP-----GLPPLWPEQ 817

206 -----SVREAGVPLGLPAPG-----ARRGSGASRLPLPK-----RPRGA 242

818 PGLVAPAPAPAAAGAPSGLPAGSGSPASSTKSSSTKSSGSGVASSPAAGP 877

243 ABEPEPTPVGGGSMHAPGTRGSDRGFCVSPAP--AEERTSLSE-ALSGTRHSPSV 299

878 DPAPER-----RKKRRAPGAR-----RPGGEEDEEGSGALGDGHD- 919

300 GRCOHNGPSTSRP-----PRPMDTCPPIVATKTFLYSGCKEQLRSPFLSLRPSLT 355

920 -DEBDGPRKRRSLGLGAP--DAFALSSSS-----SSSDDLR-----RP--- 961

356 GARLVETIFLGRPMWPGTFRRLPLRPQRYQMRPLFLLEIGNHAQCPYGLLKTGCP 415

962 -----LGPMEHPAPDGGFRVPAG-----ETHTPPSEALAAAYCP- 998

416 RAAVTPAAGVAREKQGVAAPEE-----DTDPRLVQLRGHSPWQVYGFV 465

999 -----PEVARALVDQVPEELMRPALTFDPALAHIAARRGAPLRRRA-- 1041

RESULT 22

S50832

atrophin-1 - human

C/Species: Homo sapiens (man)

C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 07-May-1999

C/Accession: S50832

R/Nagatuchi, S.; Yanagisawa, H.; Ohaki, E.; Shitayama, T.; Tadokoro, K.; Inoue, T.; Yan

Nature Genet. 8, 177-181, 1994

A/Title: Structure and expression of the gene responsible for the triplet repeat disorde

A/Reference number: S50832; MUID:95144175; PMID:7842016

A/Accession: S50832

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1184 <NAG>

A/Cross-references: EMBL:D31840

C/Genetics:

A/Status: GDB:DRP1A: 537

A/Cross-references: GDB:270336; OXIM:125370

A/Map position: 12p13.31-12p13.3112P-12P

Query Match

Best Local Similarity 22.6%; Score 130.5; DB 2; Length 1184;

Matches 88; Conservative 23; Mismatches 154; Indels 125; Gaps 16;

162 VAPSCAYVCGEPPLVQLGATQARPPH-----ASGRRLRGGERAMNHVRA 210

189 VTPGVYAPMEPTSTSMFQAPGAPPHPOLYFGTGVLGSP----- 231

211 GVPLGLPAPARRR--GGSASRSPLPKRP-----RRGAAP-EPERTPVGGSWAHAG 260

232 --FMGRGGGAASVGGPNQKHPPPTPTISVSSGAGAPPTKPTTPVGGN----- 284

261 RTGSPDRGFCVSPAPAEATSLGALSGTRHSPVGRQNHG----- 306

285 LPAPPPANPHVTPMLPAPPALR--PLNNSASPPGLGAQPLPGLHPSPYAMGQXG 341

307 -----PPTSRPPRPMDTCPPIVATKTFLYSGCKEQLRSPFLSLRPSLT 354

342 LPGPPEKPTLASPHSLPAPASSAPAPM-----RFPYSSSSSSAAAS-----SSSSSSS 393

355 TGARLVETIFLGRPMWPGTFRRL-----PLP-QRYQMRPLFLLEIGNHAQ 402

394 SSASPPFASQALPSYHSPFPPTSLSVSNQPKYTPSLPSQAVWSQGP-----PPP 445

403 CPYGVLLKTHCPLRAAVTPAGVCAEKPQGVAAPEEEDTDPRLRVQLLRQH---SSPW 459

446 PYYGRLLANSNAHPGFPSTGAQTAHPVSTHHHHHQQQQQQQQQQQCHHNSGF- 504

460 QVYGFVAPACLRLLVPPGLW-----GSRHN 483

505 -----PPGAFPHPLEGGSSHH 521

RESULT 23

T113049

eyelid - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T113049

R/Teisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.

submitted to the EMBL Data Library, March 1998

A/Reference number: Z17592

A/Accession: T113049

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-2715 <TRE>

A/Cross-references: UNIPROT:Q8IN94; EMBL:AF053091; NID:G2981220; PID:G2981221; PIDN:AA06

C/Genetics:

A/Status: GDB:DRP1A: 537

A/Cross-references: FlyBase:FBgn003013

A/Description: could act as a transcription factor antagonistic to the Wg pathway

C/Keywords: DNA binding

Query Match

Best Local Similarity 22.5%; Score 130.5; DB 2; Length 2715;

Matches 80; Conservative 29; Mismatches 140; Indels 107; Gaps 18;

173 PPLYUGAATQATQARPPHAGP---RRRLGCERA---WNHVSVEAGVPL-----GLPAPG 220

Db 1293 PPOQOQOQOQOQPPPEVGGGPPAPQOHAPGVPSPOQHVPAPACATPPPGSSGYPTPV 1352

Qy 221 ARRRGASASRLPLKRRPRGA-----APPERTPVGGGSMHAPGSTRGSPDRG 269

Db 1353 SRTPGS-----PYSPQP--GAVGYGSSDDQVYATNGPFGQPGGQGYPQNRN----- 1399

QY 270 PCVVSAPAPAEER-----TSLEGALSTRIHSHPSVG-----ROHAGPPTSTRPPPMNDT 319

Db 1400 --MYPPYGEGBEAPPGANQYGPYGSRPYSGPPPGPQPPTQTVAGGPPAGAPGAPPS 1457

QY 320 PCPPVVAETKHFHLYSSGDKE---QLRPSFLHS-----LRPSLTGAPRLVETTFIGSR 369

Db 1458 AYTGPSPQODYIQPPPDSPQPRRPDPFKDSQPIPGYNARQIYGA----- 1505

QY 370 PWWPPTPRRLRLPQ---RYWQMRPLFELLGNHACQCEYVLLKTHCPRAAVTPAGV 425

Db 1506 -WQSGTQOYRPPYSPSPAPQNWGAP-----PRGAAPPGAPHGPPIQPPAGV 1552

QY 426 CA-----REKQSGSVAAPBEDTDPRLVQLRQHSFPM-QVYGFVAACLRLLVPPG 476

Db 1553 AQMDQHRHYPPQGGPPPPQGGQPPQ---QQQQPPYQQVAG-----PPG 1593

RESULT 24

pol protein - silkworm
T18196
C/Species: Bombyx mori (silkworm)
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T18196
R/Takashi, H.; Okazaki, S.; Fujiwara, H.
Nucleic Acids Res. 25, 1578-1584, 1997
A/Title: A new family of site-specific retrotransposons SAR1, is inserted into telomeric A/Reference number: Z18809; MUID:97248614; PMID:9092665
A/Accession: T18196
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1067 (TAK)
A/Cross-references: UNIPROT:Q01419; EMBL:D85594; NID:92055274; PID:BA1976.1; PID:g205
C/Superfamily: silkworm pol protein

Query Match 2.2%; Score 130; DB 2; Length 1067;

Best Local Similarity 19.3%; Pred. No. 1.2; Mismatches 208; Conservative 89; Mismatches 306; Indels 476; Gaps 49;

QY 33 PGMRLVQSGDPAFALVAQCLVCPWDA-----RPPAPSPFOVSCIKELY 81

Db 69 PPFDFVQRG-----KGFVA-----VFMAGLLVGVYSPNRRPLAEFST--LDLGGQVY 116

QY 82 ARVLQRLCERGANVLAFGFALLDGAAGCPPEAFTTSVRSYLTNTVTDALRSGGANGLL 141

Db 117 GRSRSR-----ALVIGDLNAKSAMGSPVTCPRGRETEMLVSGSL--VVL 161

QY 142 RRVGDDVTLRLCALFVLVA-PSCAYVQCGPPLV-----QLGATQARPPHA 190

Db 162 NRGAENITVRRSGSVVDVFAIPDVARRVCGWEVLVDVETLSDHRTIGFRVAAAESSS 221

QY 191 -----SGPR--RLGCERAMNHSVREAGV-----PLGHPA--PGARRRGS 227

Db 222 VTLLPFGGVGGRWMLKLDLTER-----LQEAAYVQAWMLDLGEPADVBEAGELRRA 276

QY 228 ASR-----SLPLPKRPRRGAAPDEPERTFVGQGSWAHPQRTGSDRGCVISPARPAEAT 283

Db 277 MSFVCDVAMP-----RVRAYAPRR--QVYWNNG-----IA 305

QY 284 SLGSLSGTSHSHSVGRCHAGPPTSRPRPMDTCPPVVAETKHFHLYSSGDKEQLRP 343

Db 306 GLRRRCGSRKKYQHLRRRRRDEEDR-----AYEY-----REDVR- 344

QY 344 SFLSLSLRPSLTGA-----RLVETTFUGSRPMMGTFRRLPLPQRYWQ----- 388

Db 345 -----ARRVAIGEKAEAKMELLET--LDRDPW--GRPYLARSITKSWAPRATSTLPD 395

QY 369 -----MRPLFELLGNHACQCEYVLLKTHCPRAAVTPAGVACREKQSGVAAPEEDT 443

Db 396 IVRHVIQGLFPDAGTFPVP-----VMITPTTG-----AQIGAEDEF-- 433

QY 444 DPRELVLLRQHSSPMQVGVFVARCLRLVPPGLMGSRHNERPLRNTKFKISLGHANL 503

Db 434 -----VSPAFGAALIEKAKARRTAPGDD----- 457

QY 504 SLQELTWKMSVDCAMTRSPGVCVPAEHRRLREELIAKFLHMLMSVYVELLRSEFY 563

Db 458 -LSNRAMALA-----LQTEGGLGPV-----LRLLS-----RCRL-- 486

QY 564 TETTFQKRLFFRPSVWSKLSIGIRQHLKRVQLREISEAEVYQREARPALTSRLF 623

Db 487 -EGRP-----PEERK-----TGRVLV 501

QY 624 IPR-----PDGLRPVNDVYGARTFRREKCAEHLTSVKALGFSVLAYERARRPGL 676

Db 502 IPKEGRPHDQPSGVRPIVL-----SEAGKLREVVAGRLVRHLENY-GENLA 548

QY 677 GASV-----LGDDIHARMTFVLARVADPPPELFFVAVDVTGAVDTIROPRLTEVASII 733

Db 549 DSQGFRRGASTLDAVQVRDLSDQACSGGVLLAVSIDISNAENTVPMSTILE----- 602

QY 734 KPNTYCVRYAYVQKAAHGVKAFKSHVSTLTDLPYMKQFVAHLQETSPLRDVAVIE 793

Db 603 ----- 602

QY 794 QSSSLNEMSSGLFDVFLRFMCHAV-----RIRKSYVQCGIPQGSILSTLCS----- 843

Db 603 -SLRFRVPTGLRNLIEDYLAGRAVVPERRGWMGHKAVSC-GVPGSVLGEPLMDVGFDW 660

QY 844 -----LCYGMENKLPAGIRRDGLLRLVDPLVLTPLHAKTFLRTLVRGV 891

Db 661 VLRGANLRGVQVICTAD-----DLVTARGDYRAS--ILAAAVATVARI 706

QY 892 PEYGVVNLKRT-VVNF-----PYDEALGCTAFVQNPAGHLPFWCGILLDTRTLEV 942

Db 707 RKLGLEVALHKSSEAVCFHPARKPPGASITIGTA--IAVRSQLKYLGIWDSRW-- 760

QY 943 QSDYSVARTISIRASVFNRRGFK-----AGNMRRKLFGLVR 979

Db 761 -----SDRHFVDVLPKLGAAALRLPNTGGGKSVKRLVIGVR 803

RESULT 25

332975
gene BCRF2 protein - human herpesvirus 4
N/Alternate names: gene BMR1 protein
C/Species: human herpesvirus 4, Epstein-Barr virus
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S32975; S02383; S32976; S32977; S32978; S32980; S32981; S32982; S32983; S32984; S32985; S32986; S32987; S32988; S32989; S32990; S32991; S32992; S32993; S32994; S32995; S32996; S32997; S32998; S32999; S33000; S33001; S33002; S33003; S33004; S33005; S33006; S33007; S33008; S33009; S33010; S33011; S33012; S33013; S33014; S33015; S33016; S33017; S33018; S33019; S33020; S33021; S33022; S33023; S33024; S33025; S33026; S33027; S33028; S33029; S33030; S33031; S33032; S33033; S33034; S33035; S33036; S33037; S33038; S33039; S33040; S33041; S33042; S33043; S33044; S33045; S33046; S33047; S33048; S33049; S33050; S33051; S33052; S33053; S33054; S33055; S33056; S33057; S33058; S33059; S33060; S33061; S33062; S33063; S33064; S33065; S33066; S33067; S33068; S33069; S33070; S33071; S33072; S33073; S33074; S33075; S33076; S33077; S33078; S33079; S33080; S33081; S33082; S33083; S33084; S33085; S33086; S33087; S33088; S33089; S33090; S33091; S33092; S33093; S33094; S33095; S33096; S33097; S33098; 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S34224; S34225; S34226; S34227; S34228; S34229; S34230; S34231; S34232; S34233; S34234; S34235; S34236; S34237; S34238; S34239; S34240; S34241; S34242; S34243; S34244; S34245; S34246; S34247; S34248; S34249; S34250; S34251; S34252; S34253; S34254; S34255; S34256; S34257; S34258; S34259; S34260; S34261; S34262; S34263; S34264; S34265; S34266; S34267; S34268; S34269; S34270; S34271; S34272; S34273; S34274; S34275; S34276; S34277; S34278; S34279; S34280; S34281; S34282; S34283; S34284; S34285; S34286; S34287; S34288; S34289; S34290; S34291; S34292; S34293; S34294; S34295; S34296; S34297; S34298; S34299; S34300; S34301; S34302; S34303; S34304; S34305; S34306; S34307; S34308; S34309; S34310; S34311; S34312; S34313; S34314; S34315; S34316; S34317; S34318; S34319; S34320; S34321; S34322; S34323; S34324; S34325; S34326; S34327; S34328; S34329; S34330; S34331; S34332; S34333; S34334; S34335; S34336; S34337; S34338;

Db 676 INPCFTLKLSPVTARIELE-----GVLD-----QSQAKYLG1 710
 QY 953 STRASTENRGFKK 966
 Db 711 TLDRKLTGPHLKA 724

RESULT 28

hypothetical protein, 69k - turnip yellow mosaic virus
 C/Species: turnip yellow mosaic virus, TYMV
 C/Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C/Accession: S01955
 R/Morch, M.D.; Boyer, J.C.; Haenni, A.L.
 Nucleic Acids Res. 16, 6157-6173, 1998
 A/Title: Overlapping open reading frames revealed by complete nucleotide sequencing of t
 A/Reference number: S01955; MUID:8829359; PMID:3393388
 A/Accession: S01955
 A/Status: preliminary
 A/Molecule type: genomic RNA
 A/Residues: 1-628 <MOR>
 A/Cross-references: UNIPROT:P10357; EMBL:X07441; NID:962222; PIDN:CA0321.1; PID:962223
 A/Note: the authors translated the codon ACG for residue 459 as U
 C/Superfamily: Hydroxypoline-rich glycoprotein

Query Match 2.2%; Score 128.5; DB 2; Length 628;
 Best Local Similarity 27.6%; Pred. No. 0.73;
 Matches 89; Conservative 21; Mismatches 130; Indels 83; Gaps 18;

QY 172 GPPLYLGATQAPPPHNS-GRRRLGGERAMNHSVREGVGLG-----PAPGARRG 225
 Db 157 GPVLTETKPTVSQPRSATRG-----SFRPLLRKVHVHDDPHSSLLRR 204
 QY 226 GSASRSI-----PL-----PKRP-----RGAPPEPERPVGGGSAHPG 260
 Db 205 GSASRQOPTVRRLAPNPHSRQPPPLSDDPGLGPPPLAFHSTRD-----PP 256
 QY 261 R--TRGPD-----RGFCVSPAPPAEATSLGALSGTRHSHPSVSGQHAGPSTSRPP 314
 Db 257 RPTTPGSGNTHDLRLSLVLRTPSR-----RGILPFRHRHRTSG---HIPPTTSRPT 307
 QY 315 RPPMDPCPPVYAEKKEFLVSSGXELRPSFL-----LSSLRPSLTGARLVERTFIGSRP 370
 Db 308 GP-----PSRLQRPVHLVYSSPHTNFRPSIRKDALLLQGPRLGHERGQGANLRTSE 362
 QY 371 WMGTPRRRLPLPQRYWQMRPPLFLELIG--NHAQCPYGVLLKTHCPLRA-AVTPAAGVC 426
 Db 363 RSPPTKRLRLPRSSPNRLPKPLPEATLAPSYRHR--PYPLPMPALPSIATYSRGI 421
 QY 427 AREKQGSVAAPER-EDTPRRL 448
 Db 422 HHSLPKG--ALPKGAPPPRRL 442

RESULT 29

adenine deaminase-related protein - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: C75580
 R/White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uitterback, T.; Zalewski, C.; Ma
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: C75580
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-576 <WHI>
 A/Cross-references: UNIPROT:Q9RYP2; GB:AEO01863; GB:AEO01825; NID:96460670; PIDN:AAFI237
 A/Experimental source: strain R1

C/Genetics:
 A/Gene: DRA0268
 A/Map position: 2

Query Match 2.1%; Score 128; DB 2; Length 376;
 Best Local Similarity 25.1%; Pred. No. 0.35; Mismatches 123; Indels 150; Gaps 20;
 Matches 99; Conservative 23;

QY 3 RAPRCRAVRSLLRSYREVLPLATFVRRLGPGWELVQRGDPAAPALVAQCLVCVMDA 62
 Db 93 RADAAGRGSAAGARYRI-----LGPAP-----PRGDR-----PWS 125
 QY 63 RPPPAPEFRVYSCIKELVAVLQRLBERGAXVLAAGFALLDAG-----GPEPAF 115
 Db 126 RRLRAAARLATL-----RGAGN-----LRGRKSAARRDAPPARW 161
 QY 116 TTSVRSYLPNTVTALRSGAMGLLRVGDVLVHLARCALFVLAAPGAYVCGPPL 175
 Db 162 RRRPRAEL-----GRG-----HLRSAL-----AAPVSRPDR 191
 QY 176 YQGAATGAPPPHNSGRRRLGGER-----AMNHSVREGVPLGLPAP 219
 Db 192 HRACAGGRRRP-----AGRRRLPARRRVVELDVQRPARRHGHQSAFRAS---GGPAR 245
 QY 220 GARR-----RGASASISLPLPKRPPRGAPEPERPVGGGSAHP-----GSTR---GPSDRGFC 271
 Db 246 RQRGPARGGSGGARRRRRPGRRGPPRAVAPALRQSDDRPASGGRRCFGDGG-- 303
 QY 272 VVSPAPAEATSLGALSGTRHSHPSVSGQHAGPSTSRPPMDTPCPVYAEKGF 331
 Db 304 -----GALAGL-----HLASRHH-----PEFSRPEBDSGADAPARPDG 341
 QY 332 LYSGGDKQLRPS-----FLSSLRPSL--TGAR 358
 Db 342 VALAGPRVRRPFSAPALHLITARPVRHTGQ 376

RESULT 30

G86280
 protein T5E21.13 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: G86280
 R/theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 anen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.B.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Matzali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schreiber, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
 ket, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: G86280
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1776 <STO>
 A/Cross-references: UNIPROT:Q9MA20; GB:AEO05172; NID:97527720; PIDN:AAFI3169.1; GSPDB:GNK
 C/Genetics:
 A/Gene: T5E21.13
 A/Map position: 1

Query Match 2.1%; Score 128; DB 2; Length 1776;
 Best Local Similarity 21.8%; Pred. No. 0.33; Mismatches 204; Indels 204; Gaps 33;
 Matches 131; Conservative 63;

QY 252 GGGSAHPGRRTRGPDSDRCFVVSAPPAEATSLGALSGTRHSHPSVGRQHH-----G 306
 Db 664 GDGVYGDPSFPGPA-----AFPPPRP-----GVPTVAPLPPLPPQALNLNLRP 706
 QY 307 PPTSRP--PRPMDP-CPVYAEKKEFLVSSGXELRPSFLSSLRPSLTGARLVEI 363

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Db 707 PPSVYEGAPRRPLGVPMQPMYQQ--HQLSMGPHG--HPSMMMSR--PPQMGPMRV--- 758
QY 364 IFLGSPKMPGTPRRRLPLPQRYWQMRPLFELLNHAQCPYVLLKTHCPRAAVTPAA 423
Db 759 -----PPPPGQFSIMQVPPQYQQLPLSMGM-----QPPMAEMP-- 796
QY 424 GVCAREKPGGSVAAPPEEDTDPR-----LV-----QLRQSSPMQYGFVACRLV 473
Db 797 -----PPPPGEAPPLPEEPPEKROKLDLSALVPEDQFLACHPG-----AIIKRSK 843
QY 474 PGLWGRNHERFLNNTKFTIS--LG-----KHAKLSQELTWKMSV 514
Db 844 P-----NENDQVMEITVQSLSENVSLKEXIAGEMQIPANKQKRNPTVFERTW----- 893
QY 515 RDCAMLRBPQVGVPAAEHLREEI--LAKFLMMSVYV-----VEL 556
Db 894 ---WKEIETTGPREMPFNLLIQRCGLIDVFYWPXLYVPYDALLVPCGIIIEG 949
QY 557 L-----RSFFVYETETFOKNLFY-----RPSWSKLQSIGR----- 590
Db 950 ILSLQYQWRLNGRFFRLITSREINRMFYFKQTRLMKFSMQLPLEAPPTDGK 1009
QY 591 -----QHL--KRYQAREISEAEVQHRARAPALLTSRLRFT---PKPDGLRPIYVMD- 637
Db 1010 LGPLPPSQTLDQVEBERL-QAEONNSLAPPAVAATHTRTGIHPPPD-IRITVEKTA 1067
QY 638 YVVGARTFERERAEELTSRVKALFSLVNERARRPGLGASVGLDIDHRAMPTEVLRV 697
Db 1068 QFQSKNGLEFEKRI-----IYSEKNAFNLKSS---DYHAFYKXKLTXY 1111
QY 698 RQAD-----PPPELYFVKVDYTGAYDTP---QDRLEVIASIIKQNTYC 740
Db 1112 RQONKGAOGTDDSGTTPQDGTGAADSEAGDTPQLOAFRIPSKLEAPPEEK-YT 1170
QY 741 VR 742
Db 1171 VR 1172

RESULT 31
T31425
C-terminal domain-binding protein rat4, splice form 2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31425
R:Yuryev, A.; Paturajan, M.; Litingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord
Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
A:Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts wit
A:Reference number: 221024; MUID:96293459; PMID:8692929
A:Accession: T31425
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1048 <YUR>
A:Cross-references: UNIPROT:Q63627; EMBL:U49058; NID:g1438535; PID:g1438537; PIDN:AAC526
A:Experimental source: hippocampus

Query Match 2.1%; Score 127.5; DB 2; Length 1048;
Best Local Similarity 22.4%; Pred. No. 17; Mismatches 169; Indels 171; Gaps 25;
Matches 109; Conservative 38;

8 RAVRSLSRSHYR---EVLPLATFVRRLPGQWRLYQRDPAAFRAL--VAQCLVCPWDA 62
Db 472 RALQKLSRNGYKVNQKSIKIA-----WAL-NKGIKADFKQYMWELGVYIYIPD- 519
QY 63 RPPPAAPSRQVSCIKELVARVQLRCERGAKNVLAFFALLDG----- 106
Db 520 -----KVAAEELSFCEGG-----MLSDTLNPDWGIKPKKEN 553
QY 107 -ARGPPEAFTTSVRSYLVNTVDALRGSGAMGLLRVGDVDVLLHLLACALFVIVAP 164
Db 554 EVAQNGGAEASHTEVSPKPKV-----PPVPAALPPPAITVPPP 594
QY 165 SCAYVCCGPLYQLDAIQAQAPPPPHASGPRRLGCERAMNSVSEAGVPLGLPAPGAR 224

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Db 595 QVPPHQGPVV--VGA---LQPP--AFTP-----FLGIDPPRF-- 625
QY 225 GGSASRLPLPKRPRGAADEPERTVGGQSWAHGRTGSPDRGCVVSPAPAEATS 284
Db 626 -GQVPPPPPPPPPPGCGFPMHLPPG--FLPPG-PPPIPIPPVSIPIPPPISTIN 680
QY 285 LEGALSGTRSHSPVGRQNHAGPSTSRPRPMDTCEPVVYETKHFILYSSGDKQLRPS 344
Db 681 LVGARGNABASADSAMKYSAGPPAA-----PISLPTFPV--TQVSLITQC---VADG 730
QY 345 FLISLRPSLTGARLVERITFLGSRPM-----PGTP-----RLPLRQRYWQMRPLF 394
Db 731 PVIQLOAPs-----TGILGGRPLIPLQRPQMPPHLQRFPMMPR--PMPFHM 779
QY 395 ELIGNAQCPYVULKTHCPRAAVTPAAGVCAKEKQGSVAAP-----BE 440
Db 780 ---HRGPPG-----PGFAMPPPHGMKGPFPFHGPVRRPGMPLGCPGPGGS 827
QY 441 EDTPRR 447
Db 828 EDRDGRQ 834

RESULT 32
S22373
Proline-rich protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S22373
R:Dayfield, R.; Bannister, A.J.; Pierce, E.J.; McDonald, C.J.
Eur. J. Biochem. 204, 591-597, 1992
A:Title: cDNA clones for mouse parotid proline-rich proteins. mRNA regulation by isopren
A:Reference number: S22373; MUID:92174915; PMID:1339347
A:Accession: S22373
A:Molecule type: mRNA
A:Residues: 1-260 <LAY>
A:Cross-references: UNIPROT:Q64306; EMBL:X63004; NID:g53798; PIDN:CAA44733.1; PID:g53799
C:Superfamily: proline-rich protein

Query Match 2.1%; Score 127; DB 2; Length 260;
Best Local Similarity 27.1%; Pred. No. 0.27; Mismatches 56; Conservative 18; Mismatches 73; Indels 60; Gaps 12;
Matches 56;

172 GPLVYLGAATQARP-----PHASGPRRLGCERAMNSV-----R 208
Db 81 GPP--PQGSQQRPPQPGNQGGPPPGQPQ---GPPRPGNQVPPPEQSGQRPQPGNQ 135
QY 209 EAGVPLGLAPGAR---RQGSASRLPLPKRPRGAADEPERTVGGQSWAHGRTG 264
Db 136 QGPPPGGPRPRGQGGPPPGQPQ---PSRPGNQGGPPPGQP---QGRPPGQNGQ 188
QY 265 PSDRGFCVVSAPAPAEATSLGALSSTRHSPVGRQHAGP---STRPRPMDTFC 321
Db 189 PFPQGGPQGGPQGGNQGGPPPGQPQ---PRGNGQ--GPPPGQGPQRPQGNHG 242
QY 322 PPVYATKHFIVSSGDKQLRPSFLS 348
Db 243 PPGY-----GNNEQ--PSYLWS 257

RESULT 33
S72273
actin-depolymerizing protein N-WASP, brain - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 23-Apr-1998 #sequence_revision 01-May-1998 #text_change 09-Jul-2004
C:Accession: S72273
R:Miki, H.; Miura, K.; Takenawa, T.
EMBO J. 15, 5326-5335, 1996
A:Title: N-WASP, a novel actin-depolymerizing protein, regulates the cortical cytoskeleton
A:Reference number: S72273; MUID:97050838; PMID:8895577
A:Accession: S72273
A>Status: nucleic acid sequence not shown

```

A;Molecule type: mRNA
 A;Residues: 1-505 <MIK>
 A;Cross-references: UNIPROT:Q95107; EMBL:D67066; NID:G1644231; PIDN:BA11082.1; PID:dl01
 A;Experimental source: brain

Query Match 2.1%; Score 127; DB 2; Length 505;
 Best Local Similarity 24.7%; Pred. No. 0.69; Indels 112; Gaps 14;
 Matches 74; Conservative 17; Mismatches 97

173 PPVQLGATQAPPPPPASGPRRRRLGGERAMNSVBAAGVFLGLPAPGARRRG----- 226
 279 PPPPSRGPPPPPPPPHSSGP-----PPPPARGGAPPPPS 315
 Db
 227 ---SASRSLPLPKRRPGAGAPPEPRRTVCGGSMANHGRTGSPDRGFCVSPAPRABEAT 283
 316 RAPTAAPPPPPPPPPGVGAPPP-----PPRMPPPP-----LPALPS----- 352
 Db
 284 SLEGALSGTRHSHPSVGRQHAGPPSTRRPRMDTPCPVVAETKHFLVSSGDKQLRP 343
 353 ---SAPGCPPPPPPPPLSVSGSVAPPPPPPPPPGPPPP-----GLPSGDHQVPTP 402
 QY
 344 ---SFLSSLRPSLTARLVETIFLGSPPMPGCTPRRLPLPQKRWQKPLFLELGN 399
 403 AGSKPALLDIIR---EGAO---LKKEVQNSRP-----VSCGSR 434
 Db
 400 HA---QCPYGVTLK---THCP---LRAAVTPAAGVCA-----REKQGSVAAPPEEDPD 444
 435 DALLDQIRQGIQLKSVTDAPESTPPAPAPTSIGVGLMEVMQKRSKRIHSDDEDDEDD 494

RESULT 34
 T43481
 probable mucin DKFZp434C196.1 - human (fragment)
 N;Alternate names: protein DKFZp434B035.1
 C;Species: Homo sapiens (man)
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T43481; T34549; T17264
 R;Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, December 1999
 A;Reference number: Z22514
 A;Accession: T43481
 A;Molecule type: mRNA
 A;Residues: 1-580 <AAA>
 A;Cross-references: UNIPROT:Q9UF83; EMBL:AL133561; NID:G6599133; PIDN:CAB63715.1; PID:G6
 R;Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, October 1999
 A;Reference number: Z21540
 A;Accession: T34549
 A;Molecule type: mRNA
 A;Residues: 262-580 <POU2>
 A;Cross-references: EMBL:AL12069; NID:G6102864; PIDN:CAB59245.2; PID:G7018420
 R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, September 1999
 A;Reference number: Z18723
 A;Accession: T17264
 A;Molecule type: mRNA
 A;Residues: 262-580 <POU2>
 A;Cross-references: EMBL:AL117481; NID:G5911958; PIDN:CAB5954.1; PID:G5911959
 C;Experimental source: adult testis; clone DKFZp434B061
 C;Genetics: A;Note: DKFZp434C196.1; DKFZp434B0635.1; DKFZp434B061.1

Query Match 2.1%; Score 127; DB 2; Length 580;
 Best Local Similarity 26.6%; Pred. No. 0.83;
 Matches 74; Conservative 18; Mismatches 110; Indels 76; Gaps 13;

141 LRRVGDVVLVHLLARCALFVLVAPSCAYQVCPULYQLGATQARPPPHAS-----CP 133
 52 LTKHESTALLTLTPASL---WRTPTRASLWRTTP---RASPTPKPPRASPTPSASP 104
 QY
 194 RRLGCEBAMNSVBAAGVFLGLPAPGARRRGASASRLPLPKSPRRGAAPPEE-RTPVG 252

Db
 105 TRRL-----PRASPM-----GSPHASAPRTTPRASPTGPTASTPTG 142
 QY
 253 QGSMANPRT-----RPSDRGFCVSPAPRABEATLSEAL-----SGTRHSHPSV 299
 Db
 143 TPSSASPTGTPPPASPTGTPPRAMATRSSPTASLRTPTSSRASLTRWPPRASPTTPPPES 202
 QY
 300 GQGHAGPPS-----TSRPPRPMWDPCEPVVAETKHFLVSSGDKQLRPFLSLSLR 351
 203 PRMSHRASPTTPPPASPTKRPPPASPTTPP-----RESULTSHASPTR 248
 Db
 352 --PSLTGARLVETIFLGSRP--WMPGT--PRRLPLPQR 365
 249 MPPRASPTRRPPRASPTGSPPRASPMTPPRASPTTPR 286

RESULT 35
 A53800
 mixed-lineage protein kinase (EC 2.7.1.-) 3 - human
 N;Alternate names: protein kinase PTK1; protein kinase SPRK
 C;Species: Homo sapiens (man)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: A53800; I58395
 R;Gallo, K.A.; Marx, W.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
 J. Biol. Chem. 269, 15092-15100, 1994
 A;Title: Identification and characterization of SPRK, a novel src-homology 3 domain-conte
 A;Reference number: A53800; MUID:94253068; PMID:8195146
 A;Accession: A53800
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-847 <GAU>
 A;Cross-references: UNIPROT:Q16584; GB:U07747; NID:G464027; PIDN:AA19647.1; PID:G464028
 R;King, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassar, N.J.
 Oncogene 9, 1745-1750, 1994
 A;Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 domain
 A;Reference number: I58395; MUID:94239754; PMID:8185572
 A;Accession: I58395
 A;Molecule type: mRNA
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Residues: 1-847 <RES>
 A;Cross-references: GB:I12976; NID:G488295; PIDN:AAA59659.1; PID:G488296
 C;Genetics: A;Gene: GDB:MLK3; PTK1; SPRK
 A;Cross-references: GDB:I34755; OMTW:600050
 A;Map position: 11413.1-11413.3
 C;Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
 K;Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein ki
 F;48-100/Domain: SH3 homology <SH32>
 F;115-383/Domain: protein kinase homology <KIN>
 F;123-131/Region: protein kinase ATP-binding motif
 F;403-424/Region: leucine zipper motif
 F;438-459/Region: leucine zipper motif
 F;468-482/Region: basic

Query Match 2.1%; Score 127; DB 1; Length 847;
 Best Local Similarity 23.1%; Pred. No. 1.4; Indels 178; Gaps 34;
 Matches 122; Conservative 49; Mismatches 179

QY
 44 PAAPRALVAQCLVCEWMDARPPPAASFRQV-SCIKELVARYLQL-----CERGAN 95
 346 PEPFAQLMADC-----W-AQDPHRRPDDASIIQQLALEAQLTRMPDPSFMSQEGWKR 401
 Db
 96 VLAFFALLDGARG-----GPEAFTTSVRSYLNTYTDALRGS-----GAW----- 137
 402 EIQ---GLPDELRAKEXELLSREBELTRAR--QRQAQQLRREHLLAQHELEVFERE 456
 QY
 138 -GLLRRV-----GDDVVLHLLARCALFVLVAPSC-----A 167
 457 LTLILQGVDRERPHVRRRGTFKRSKLRAPOGGERISMDLPKIRITVQASGLDRRRNV 516
 QY
 168 YQVCGP---PLYQLGATQAR--PPHASG---PR-----LLGERAMNSVBAAG 211
 517 FEV-GPGDSPTPFRFRAIQLPEAPAEQAGROSFRLEDSNGERRAC-WAWGDS----- 569

QY 212 VPLGLPAPGARRRGSGASR-----SLPL-----PKRPRGAPAEPEPT 249
 Db 570 -----SRPBGACQGRRRSRNDEATWLDSDSPLOSPTPALNPNRPRLBEPBEG 625
 QY 250 PVQGGSMADGRTGSDRGFCVSP--ARPAEATSLGALSGTRHSPVSGQHANG 306
 Db 626 PV-----PAERGSSSGTPEKLIORALIRGTALLAGIGRDIQPGCGPREG 672
 QY 307 PSTSSPPRPMWDRPC--PYVATKHFLLSSGDKQELRSPFLSSL-----RSLTGAR 359
 Db 673 SSTT--PPTTTPAPCTTBPSPFLICSLKTPDSPP--TAPLLDLIGIVGQSAKSPR 730
 QY 360 LVE-----TFLGSRPMWPGTTPRLPRLPQRYWQMRPLELLGNHACPYVLKTH--CP 414
 Db 731 EEPFRGTV---SP--PGTSRAPGTP-----GTPSPPLGHSRPRSP 771
 QY 415 LRANVPAGVCAREKPGQSVAPAEEDDPRLVQLRGHSPQVY 462
 Db 772 LRSRIDPMSFVSAGPRP--SPLEPQDA--PR-----APWTLF 806

RESULT 36

T46289
 hypothetical protein DKFZp434A1010.1 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #ext_change 09-Jul-2004
 C/Accession: T46289
 R/Duesterhoft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A/Reference number: Z23035
 A/Accession: T46289
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-862 <AAA>
 A/Cross-references: UNIPROT:Q9NT23; EMBL:AL137579
 A/Experimental source: adult testis; clone DKFZp434A1010
 C/Genetics:
 A/Note: DKFZp434A1010.1

Query Match 2.1%; Score 127; DB 2; Length 862;
 Best Local Similarity 21.8%; Pred. No. 1.4;
 Matches 102; Conservative 28; Mismatches 147; Indels 190; Gaps 23;

QY 43 DPAAPRALVAQCLVCVPMWARP-----PAASTFQV 74
 Db 316 DEPTTR-----CSSPTGDDPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 370
 QY 75 SCLKELVARVQLRCERGAQNVLAFGFALLDGAAGCPPEAFTTSV-----RSYLPYVTVDA 130
 Db 371 S--EPLAVSVPPAVLE-----LLGAGAPAPASATPTPALSPGSLRPHLLPL 415
 QY 131 LRGSGAGMGLLRVVDVVLHARCALFVVAESCAVQCG----- 172
 Db 416 LRGAE-----PLTDACQCEMSKLRGAQGLPDMESFLP 451
 QY 173 -PPLYOL--GAATARPAPHASGPRRLG--CERAMHNSVREA-----GVPLGLPARGA 221
 Db 452 PPLSLIRRGGA-----PPPPKPNPARLMAALAAEAQVABQSGQEGCGTPPASQSPFH 507
 QY 222 RRRGASASGLPLPKRP--RRGAAPERTTPVQGSMAHPG----- 260
 Db 508 R-----SLSTLVGGEPLGTSGSGPPF-----NSLHAPGAWVPGPPYLPQOQSDSL 554
 QY 261 -----RTRGSDRGFCVSPAPAPAEATSLGALSGTRHSPVSGQHANGPSTSRP-- 314
 Db 555 LRSQPMGSRKGL-----RGPAQVSAQLRA--GGGAGDAEAAAGSCSVSPQVPTPBG 607
 QY 315 -RPMWTPC--PVPYATKHFLLSSGDKQELRSPFLSSLRPLTGARLVETIFLGSRPM 372
 Db 608 PSPAPRECIPLPLGVKPGIYPLGP-----PSFGSSAP-----VWR 645
 QY 373 P--GTPRRLRLPQRYWQMRPLELLGNHACCPYVLKTHCPRA 417

Db 646 SSLGPAPALDRNGENLYE-----IGASEGSPYSLTMSWSPFRS 684

RESULT 37

T35878
 hypothetical protein SC9B10.09 - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #ext_change 09-Jul-2004
 C/Accession: T35878
 R/Oliver, K.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, November 1997
 A/Reference number: Z21592
 A/Accession: T35878
 A/Status: preliminary; translated from GB/EMBL/DDJ
 A/Molecule type: DNA
 A/Residues: 1-1039 <OLI>
 A/Cross-references: UNIPROT:O50516; EMBL:AL009204; PIDN:CAAL5799.1; GSPDB:GN00070; SCODE
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: SCODEB:SC9B10.09

Query Match 2.1%; Score 127; DB 2; Length 1039;
 Best Local Similarity 26.1%; Pred. No. 1.9; Indels 80; Gaps 16;
 Matches 89; Conservative 26; Mismatches 146;

QY 4 APRCAVRSLLRSHREVLEPLATFVRLEGQGRVLYQGDPAFRALVAQCLVCVPMWARP 63
 Db 462 APQCHAVRAR-----LPHATVSALLRQAG--VIRVD--TITLDVAGLLLA--RQ 506
 QY 64 PPPAPSFQVSCLEKELVARVQLRCERGAQNVLAFGFALLDGAAGCPPEAFTTSVRS-- 121
 Db 507 PLPAPPRVALTGNSESL-----GLTYDACISGLRQPLDTTASAD 552
 QY 122 -----YLPNTVDAL-----RSGAGMGLLRVVDVVLHARCALFVVAESCA 167
 Db 553 FHAAALBALADTCDVAVVTAIPTLGEA-----AGDAALAEALRSAAAAPVTPPVLY 605
 QY 168 YQVCGPELVOLGAATQARPAPHASGPRRLG--CERAMHNSVREAQVPLGLPA--PGAR 222
 Db 606 VHV-----ELGGLAALSAATASTAPQTAGTAAEGASRAASAAALPADPDVAV 659
 QY 223 RRGASASRLPLPKRRRGAPAPERTTPVQGSMAHPGTRGSDRGFCVSPAPAPAEBA 282
 Db 660 RRG-----TSGASAGAPASGATP--GTAPHAP--GPAQD--LPSGASGSPGP 703
 QY 283 TSLEALSGTRHSPVSGQHANGPSTSRPAPMDTCP 323
 Db 704 SCPSGSPGSGPSPGSPS--GPSGSPGSPGSPGPPRPSAPGRP 743

RESULT 38

H75272
 probable nucleic acid-binding protein, HRDC family - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #ext_change 09-Jul-2004
 C/Accession: H75272
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M., Shen, M.; Vamathevan, J.U.; Lam, P.; McDonald, L.; Uitterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; WUID:20036896; PMID:10567266
 A/Accession: H75272
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-603 <MHI>
 A/Cross-references: UNIPROT:Q9RPD4; GB:AE002074; GB:AE000513; NID:G6460257; PIDN:AAFI1987
 A/Experimental source: strain R1
 C/Genetics:
 A/Gene: DR2444
 A/Map position: 1

Query Match 2.1%; Score 126.5; DB 2; Length 603;
 Best Local Similarity 25.0%; Pred. No. 0.95;
 Matches 131; Conservative 39; Mismatches 184; Indels 171; Gaps 32;

QY 37 RLNVQ---RGDPAAFRALVAQCLVGVWDARPPPAAPSPQVSC-LKELVARYLQRLCER 91
 DB 12 RLNVQLHNERDDPGRLLAALAALEDTEWGLLAGBALAQALALGPGLRVDRGL-DY 70
 QY 92 GAKNVLAFGALDD-----GARG---GPPPAFTTSVRSYLPTYTDA-LRSSGAMGLL 140
 DB 71 GRAALABAGLAVADLHGDLAGARAVWLEBPRAAVERARAGRVYVADATLARGGM--- 127
 QY 141 LRRVGDVVLVHLARCAFLVVAAPSCAYQVCGPPLYQAGAA-TQARPPEH----- 189
 DB 128 -PRGADYVYVRNAYVITLGHADAPLAA-----LFGSGTAPTPAAPPPSDIALVALALND 179
 QY 190 -ASGPRF-----RLGGERAMNSVREAGVPLCPAPGA---RRRG- -SA 228
 DB 180 VALPLRLAFAFARTATQTLTRLGA-----SVRQAGFTALLLPDSADTPAQLGVLAA 233
 QY 229 SRSLEP-----LPRRRGAAPPEPRTVGGGSMNHPGRTGSPSDRGF 270
 DB 234 ARHVFDGLLTPGLEDEPOVGLLRDQPE---ARRQDQASGGGSEASQ--REGQORDER 287
 QY 271 CVVSPAPPAEATSLLEGALSGTRSHSPSVGRONHAGPPSTSRPPRPMDTPCPPEVYAEIKH 330
 DB 288 -QNRVEDRPRONA---EGRAPADREDRPERSEORVSPERSRDRPREDR---FRDDR 339
 QY 331 FLVSSGKEQLRPSFLSSLRPSLTGARLVETIFLGSRPMWGTERRRLPRL---PQRY 386
 DB 340 ---REGRRDRFRBS--EGPRPRTTGER-----RQDAPAPAELEIRFTFEAPQQA 384
 QY 387 ---WQMRPLFLELGNHAQCPYGLIKTHC-----PL----- 415
 DB 385 PAPSBDLPWEPELVF---SDHA--PQNVPL-THVSSGSDAPPLPITPPLAOTLSEADA 437
 QY 416 ---RAAVTPAAGVCARE-----KQGSVAABEEDTDP 446
 DB 438 GDAAGQTPAELFEVHAAPVSSAQTFEPQ--VEAPEPAEAPQ 480

RESULT 39
 E98119
 Transposase, uncharacterized, truncation [Imported] - Streptococcus pneumoniae (strain R
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: E98119
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; Dehoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.O.; Lu, J.; Matsushima, P.; Mcahren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain Re.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: E98119
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-330 <KUR>
 A:Cross-references: UNIPROT:Q8DN10; GB:AE007317; PIDN:AL00786.1; PID:G15459687; GSPDB:G
 C:Genetics:
 A:Gene: transposase H

Query Match 2.1%; Score 126; DB 2; Length 330;
 Best Local Similarity 21.8%; Pred. No. 0.45;
 Matches 46; Conservative 29; Mismatches 62; Indels 74; Gaps 4;

QY 707 YFVAVDTGAVDTIPQDRLTEVIAIKPONTYCVRRYAVYQKAHGVAKAFKSHVSTL 766
 DB 39 WIVDIDLEKFPDIPQDRIMSLVNIITLEDGT----- 70
 QY 767 TDLQPMQFVAHLQETSPLRDAAVVIQSSSLNEASSGLFDVPLRMCHAVNIRKSYI 826
 DB 71 -----ESLIRKYLHSGVILINGORYK 90

QY 827 OCGIFQGSIIISTLLCSLCYGDMEKLFAGIRBDL-LRLVDDPLVTPHITAKITLR 885
 DB 91 TLVGTPOGNSLSPILSN-----MLNELDELEKRLRFVYADDCVITVSEAAKRMVY 146
 QY 886 TLVRGVPF-YGCVNLARKTVNFPVEDEALG 915
 DB 147 SVSRFIEKRLGLKVMVMTKTKITRRELKYL 177

RESULT 40
 T43556
 Wiskott-Aldrich syndrome protein homolog - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T43556
 R:Zankel, T.C.; Ow, D.W.
 submitted to the EMBL Data Library, December 1997
 A:Description: A Wiskott-Aldrich Syndrome protein homolog in Schizosaccharomyces pombe,
 A:Reference number: 222575
 A:Accession: T43556
 A:Status: preliminary; translated from GB/EMBL/DBU
 A:Molecule type: DNA
 A:Residues: 1-574 <ZAN>
 A:Cross-references: UNIPROT:O36027; EMBL:AF038575; PIDN:AAB92587.1
 A:Experimental source: strain J521
 C:Genetics:
 A:Gene: wsp1
 A:Map position: I
 A:Introns: 72/3; 519/3; 564/1

Query Match 2.1%; Score 125.5; DB 2; Length 574;
 Best Local Similarity 25.7%; Pred. No. 1;
 Matches 72; Conservative 16; Mismatches 107; Indels 85; Gaps 12;

QY 173 PPLYQLGATQA---RPPHAGSRRRLGGERAMNSVREAGVPLGLPAGARRGSA 228
 DB 294 PSSRSVSAALAAANKRRPPPPPPRRNRGKPPICNGSSNSLPP---PPPPR---SNA 347
 QY 229 SRSLEPFRPRGAAPPEPRTVGGGVAHPGRTGSPSDRGFCVVSPAPPAEATSLGGA 288
 DB 348 AGSTLPPQGRASAPPPPPR-----SAPSTGRQPPPLSSSRASNPAPP----- 392
 QY 289 LSGTRHSHPSV-GROHAGPP-----STSRPPRPMDTPCPPEVYAEIKHFLYSSGDKQLR 342
 DB 393 -----PAIPGRSAPALPPLGNASRTSTPPVPPLP-----SA 427
 QY 343 PEFILSLRPSLTGARLVETIFLGSRPMWGTERRRLPRLPQRYWQMPLELIGNHAQ 402
 DB 428 PPSLPPSAPPPLP-----MGA-PAPPLPSSAIIAP-----PL----- 459
 QY 403 CEYGLLTKHCPRLRAAVTPAAGVCAREKPGQSVAAPEED 442
 DB 460 -PAGMPAAPPLPPAPAPPAPAPAPAPAVASIALPQOD 498

Search completed: December 20, 2004, 16:01:06
 Job time : 40 secs

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